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Shears, Beverly

From: Hamud, Fozia
Sent: Monday, August 18, 2003 12:36 PM
To: Shears, Beverly
Subject: RE: Seq. Search Request

Sorry about that. It is SEQ ID NO:2. Thanks.

-----Original Message-----

From: Shears, Beverly
Sent: Monday, August 18, 2003 12:34 PM
To: Hamud, Fozia
Subject: Seq. Search Request

Fozia,

You recently submitted a seq. search request for SN 09/892949; however, you omitted the Seq. ID to be searched. Your request reads:

Pls. search SEQ ID NO:from amino acid residue 20-227; 544-732; 520-543 against commercial data bases. thanks.

Which Seq. ID do you wish to search?

BEVERLY SHEARS
USPTO
BIOTECH/CHEM LIBRARY
CM-1, RM 1E05
703-308-4994
BEVERLY.SHEARS@USPTO.GOV

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Hamud F.
09/892449 Page 1
Seq. ID 2GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 13:12:37 ; Search time 79.0499 Seconds
(without alignments)
417.649 Million cell updates/sec

Title: US-09-892-949-2_COPY_20_227

Perfect score: 1121

Sequence: 1 ALPAKRENISCVYYRKRLT.....SKFWSDSQEKMGTEEEAP 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues 1107863

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1121	100.0	324	23	ABR05732
2	1121	100.0	548	24	ABP54369
3	1121	100.0	549	24	ABP54368
4	1121	100.0	581	24	ABP54367
5	1121	100.0	582	23	ABR95608
6	1121	100.0	582	23	ABR95602
7	1121	100.0	582	23	AAU83637
8	1121	100.0	627	24	ABP54366
9	1121	100.0	649	23	ABR05738

10	1121	100.0	652	22	ABR51242
11	1121	100.0	652	23	AAE24028
12	1121	100.0	662	22	ABR51244
13	1121	100.0	662	23	AAE24029
14	1121	100.0	662	23	ABR05741
15	1121	100.0	681	24	ABP54363
16	1121	100.0	732	23	ABR05730
17	1121	100.0	745	23	AAE24024
18	1121	100.0	764	23	ABR05743
19	1121	100.0	764	24	ABP54364
20	1121	100.0	764	24	ABP54365
21	1110	99.0	239	23	ABR05733
22	1110	99.0	252	22	ABR51243
23	1110	99.0	252	23	AAE24027
24	502.5	44.8	547	23	ABR05745
25	502.5	44.8	662	23	ABR05742
26	502.5	44.8	716	24	ABP54370
27	502.5	44.8	716	24	ABP54371
28	502.5	44.8	726	23	AAE24037
29	295	26.3	77	23	AAE24022
30	271.5	24.2	917	13	AAV55073
31	271.5	24.2	917	21	AAV55073
32	268.5	24.0	332	20	AAW70799
33	268.5	24.0	332	21	AAV92188
34	268.5	24.0	488	22	AAE12610
35	268.5	24.0	488	23	AAE23860
36	268.5	24.0	658	17	AAE94576
37	268.5	24.0	708	17	AAE85911
38	268.5	24.0	727	21	AAV92192
39	268.5	24.0	738	21	AAV92194
40	268.5	24.0	809	23	AAV75498
41	268.5	24.0	859	20	AAW70796
42	268.5	24.0	859	21	AAV92184
43	268.5	24.0	918	12	AAE10545
44	268.5	24.0	918	15	AAE46233
45	268.5	24.0	918	17	AAE75368

ALIGNMENTS

RESULT 1
ABR05732
ID ABR05732 standard; Protein; 324 AA.
XX
AC ABR05732;
XX
DT 01-MAY-2002 (first entry)
XX
DE Zcytor17 soluble form truncated in the fibronectin domain SEQ ID NO.18.
XX
KW Zcytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;
XX
KW antiinflammatory; antiviral; antithrombotic; cytoskeletal;
XX
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
XX
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
XX
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX
KW inflammatory disease; pancreatitis; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
PN WO200200721-A2.
XX
PD 03-JAN-2002.
XX
PF 26-JUN-2001; 2001WO-US20484.
XX
PR 26-JUN-2000; 2000US-214282P.
XX
PR 29-JUN-2000; 2000US-214955P.
XX
PR 08-FEB-2001; 2001US-267963P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Presnell SR, Gao Z, Whitmore TB, Kujiiper JL;

PI Maurer MF;
XX
XX WPI: 2002-090519/12.
DR N-PSDB; ABA93781.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders -
XX
XX Claim 23; Page 176-177; 235pp; English.
XX
XX The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antineumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 324 AA;
SQ
Query Match 100.0%; Score 1121; DB 23; Length 324;
Best Local Similarity 100.0%; Pred. No. 2,7e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALPAKPNISCVYYRKNLCTWSPKETSYYQYVRYAFGEKNDCTNSTSENRA 60
DB 20 ALPAKPNISCVYYRKNLCTWSPKETSYYQYVRYAFGEKNDCTNSTSENRA 79
QY 61 SCSPFLPRITIPDNYTIEVEAENGQVYKSHMTYRLNIAKTEPPKIFRYKPVLGIKRM 120
DB 80 SCSPFLPRITIPDNYTIEVEAENGQVYKSHMTYRLNIAKTEPPKIFRYKPVLGIKRM 139
QY 121 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTGLOPTEYVI 180
DB 140 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTGLOPTEYVI 199
QY 181 ALRCVAVESKFWSDMSQEKMGTEBEAP 208
DB 200 ALRCVAVESKFWSDMSQEKMGTEBEAP 227
RESULT 2
ABP54369
ID ABP54369 standard; Protein; 548 AA.
XX
XX ABP54369;
AC
XX 20-JAN-2003 (first entry)
DT
XX
XX Human NR10.8 splicing variant protein SEQ ID NO:14.
DE
XX
XX NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation.
XX
XX Homo sapiens.
OS
XX
XX WO200277230-A1.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 22-MAR-2002; 2002WO-JP02769.
PF
XX

PR 26-MAR-2001; 2001JP-0087298.
XX
XX (CHUS) CHUGAI SEIYAKU KK.
PA
XX
XX Maeda M, Yaguchi N, Hasegawa M;
PI
XX
XX WPI: 2003-018925/01.
DR N-PSDB; ABQ83369.
XX
XX NR10 splicing variants of hematopoietin receptor proteins and encoded
PT genes; applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -
XX
XX Claim 1; Fig 19-21; 250pp; Japanese.
XX
XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietin receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.8
CC protein from the present invention.
XX
XX Sequence 548 AA;
SQ
Query Match 100.0%; Score 1121; DB 24; Length 548;
Best Local Similarity 100.0%; Pred. No. 5,7e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALPAKPNISCVYYRKNLCTWSPKETSYYQYVRYAFGEKNDCTNSTSENRA 60
DB 52 ALPAKPNISCVYYRKNLCTWSPKETSYYQYVRYAFGEKNDCTNSTSENRA 111
QY 61 SCSPFLPRITIPDNYTIEVEAENGQVYKSHMTYRLNIAKTEPPKIFRYKPVLGIKRM 120
DB 112 SCSPFLPRITIPDNYTIEVEAENGQVYKSHMTYRLNIAKTEPPKIFRYKPVLGIKRM 171
QY 121 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTGLOPTEYVI 180
DB 172 IOIEWIKPELAPVSSDLKYLRFRTVNSTSWMEVNFANRDKNQYVNLTGLOPTEYVI 231
QY 181 ALRCVAVESKFWSDMSQEKMGTEBEAP 208
DB 232 ALRCVAVESKFWSDMSQEKMGTEBEAP 259
RESULT 3
ABP54368
ID ABP54368 standard; Protein; 549 AA.
XX
XX ABP54368;
AC
XX 20-JAN-2003 (first entry)
DT
XX
XX Human NR10.7 splicing variant protein SEQ ID NO:12.
DE
XX
XX NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation.
XX
XX Homo sapiens.
OS
XX
XX WO200277230-A1.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 22-MAR-2002; 2002WO-JP02769.
PF
XX
XX 26-MAR-2001; 2001JP-0087298.
PR
XX
XX (CHUS) CHUGAI SEIYAKU KK.
PA

XX Maeda M, Yaguchi N, Hasegawa M;
XX WPI; 2003-018925/01.
DR N-PSDB; ABQ83367.
XX
XX NR10 splicing variants of hematopoietin receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -
XX
XX Claim 1; Fig 16-18; 250pp; Japanese.
XX
XX The present invention describes hematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC hematopoietic factors, and developing remedies for immunological and
CC hematopoietic diseases. The hematopoietin receptor genes participate
CC in in vivo immunomodulation and hematopoietic cell regulation, and in
CC the search for hematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.7.
CC protein from the present invention.

XX Sequence 549 AA;

Query Match 100.0%; Score 1121; DB 24; Length 549;
Best Local Similarity 100.0%; Pred. No. 5,7e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 60
DB 52 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 111
QY 61 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 120
DB 112 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 171
QY 121 IQIEWIKPELAPVSSDLKYLFRFTVNSTSMVEVNFANRDKNQYTNLTGLQPTFEYVI 180
DB 172 IQIEWIKPELAPVSSDLKYLFRFTVNSTSMVEVNFANRDKNQYTNLTGLQPTFEYVI 231
QY 181 ALRCAYESKFSWSDMSQEKMGTEBEAP 208
DB 232 ALRCAYESKFSWSDMSQEKMGTEBEAP 259

RESULT 4

ABP54367
ID ABP54367 standard; Protein; 581 AA.

XX AC ABP54367;

XX DT 20-JUN-2003 (first entry)

XX DE Human NR10.6 splicing variant protein SEQ ID NO:10.

XX KM NR10; splicing variant; hematopoietin receptor; immunomodulator;
KM haemostatic; hematopoietic factor; immunological disease;
KM hematopoietic disease; hematopoietic cell regulation.

XX OS Homo sapiens.

XX PN WO20027230-A1.

XX PD 03-OCT-2002.

XX PF 22-MAR-2002; 2002WO-JP02769.

XX PR 26-MAR-2001; 2001JP-0087298.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX Maeda M, Yaguchi N, Hasegawa M;
XX

DR WPI; 2003-018925/01.
DR N-PSDB; ABQ83367.

XX
XX NR10 splicing variants of hematopoietin receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -
XX
XX Claim 1; Fig 13-15; 250pp; Japanese.

XX The present invention describes hematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC hematopoietic factors, and developing remedies for immunological and
CC hematopoietic diseases. The hematopoietin receptor genes participate
CC in in vivo immunomodulation and hematopoietic cell regulation, and in
CC the search for hematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.6
CC protein from the present invention.

XX Sequence 581 AA;

Query Match 100.0%; Score 1121; DB 24; Length 581;
Best Local Similarity 100.0%; Pred. No. 6,2e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 60
DB 52 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYTKRYTAFGEKNDCTNSTSENRA 111
QY 61 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 120
DB 112 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYRLNIAKTEPKIFRYKPVLAGIKRM 171
QY 121 IQIEWIKPELAPVSSDLKYLFRFTVNSTSMVEVNFANRDKNQYTNLTGLQPTFEYVI 180
DB 172 IQIEWIKPELAPVSSDLKYLFRFTVNSTSMVEVNFANRDKNQYTNLTGLQPTFEYVI 231
QY 181 ALRCAYESKFSWSDMSQEKMGTEBEAP 208
DB 232 ALRCAYESKFSWSDMSQEKMGTEBEAP 259

RESULT 5

ABB95608
ID ABB95608 standard; Protein; 582 AA.

XX AC ABB95608;

XX DT 19-JUL-2002 (first entry)

XX DE Human angiogenesis related protein PRO21384 SEQ ID NO: 372.

XX KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM cardiac; cytostatic; antiangiogenic; hypotensive; vulnary;

XX KM antiarteriosclerotic.

XX OS Homo sapiens.

XX PN WO200208284-A2.

XX PD 31-JAN-2002.

XX PF 09-JUL-2001; 2001WO-US21735.

XX PR 20-JUL-2000; 2000US-219556P.

XX PR 25-JUL-2000; 2000US-220624P.

XX PR 28-JUL-2000; 2000WO-US20710.

XX PR 02-AUG-2000; 2000US-222695P.

XX PR 17-AUG-2000; 2000US-0643657.

XX PR 23-AUG-2000; 2000WO-US23322.

XX PR 24-AUG-2000; 2000WO-US23328.

PR	07-SEP-2000,	2000US-230978P.
PR	15-SEP-2000,	2000US-000000P.
PR	18-SEP-2000,	2000US-0664610.
PR	18-SEP-2000,	2000US-0665350.
PR	24-OCT-2000,	2000US-242922P.
PR	08-NOV-2000,	2000US-0709238.
PR	08-NOV-2000,	2000WO-US30952.
PR	10-NOV-2000,	2000WO-US30873.
PR	01-DEC-2000,	2000WO-US32678.
PR	20-DEC-2000,	2000US-0747259.
PR	20-DEC-2000,	2000WO-US34956.
PR	22-JAN-2001,	2001US-0767609.
PR	28-FEB-2001,	2001US-0796498.
PR	28-FEB-2001,	2001WO-US06520.
PR	01-MAR-2001,	2001WO-US06666.
PR	09-MAR-2001,	2001US-0802706.
PR	14-MAR-2001,	2001US-0806689.
PR	22-MAR-2001,	2001US-0816744.
PR	05-APR-2001,	2001US-0828366.
PR	10-MAY-2001,	2001US-0854208.
PR	10-MAY-2001,	2001US-0854280.
PR	25-MAY-2001,	2001US-0866028.
PR	25-MAY-2001,	2001US-0866034.
PR	25-MAY-2001,	2001WO-US17092.
PR	30-MAY-2001,	2001US-0870574.
PR	01-JUN-2001,	2001WO-US17443.
PR	01-JUN-2001,	2001WO-US17800.
PR	20-JUN-2001,	2001WO-US19692.
PR	28-JUN-2001,	2001WO-US00000.

PA	(GETH) GENTECH INC.
PA	(BAKE) BAKER K P.
PA	(FERR) FERRARA N.
PA	(GERB) GERBER H.
PA	(GERR) GERRITSEN M E.
PA	(GODD) GODDARD A.
PA	(GODO) GODOWSKI P J.
PA	(GURN) GURNEY A L.
PA	(HILL) HILLAN K J.
PA	(MARS) MARSTERS S A.
PA	(PANU) PANI J.
PA	(PAON) PAONI N F.
PA	(STEP) STEPHAN J F.
PA	(WATA) WATANABE C K.
PA	(WILL) WILLIAMS P M.
PA	(WOOD) WOOD W I.
XX	
XX	
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI	Godowski PJ, Gunney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX	
DR	WPI: 2002-171999/22.
DR	N-PSDB; ABL95746.
XX	
XX	
PT	One hundred and eighty seven nucleic acids encoding PRO myocardin
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infection), endothelial or angiogenic disorders in a mammal -
XX	
PS	Claim 11; Fig 372; 567dp; English.

The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and healing. The present sequence is a PRO protein of the invention.

Sequence	582 AA;
Query Match	100.0%;
Best Local Similarity	Score 1121; DB 23; Length 582; Pred. No. 6.2e-103;

	Matches	208	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	ALPAKPENISCVYYRRKRLTCTTMSPGKETSITYQTVTKRTVAFGKHNDCTNNSSTSENRA	60							
Db	52	ALPAKPENISCVYYRRKRLTCTTMSPGKETSITYQTVTKRTVAFGKHNDCTNNSSTSENRA	111							
QY	61	SCSFPLPRTTIDQVYITEVEALENDGVIKSMHTYWRLENIAKTEPPKIFRVKPIVIGIRM	120							
Db	112	SCSFPLPRTTIDQVYITEVEALENDGVIKSMHTYWRLENIAKTEPPKIFRVKPIVIGIRM	171							
QY	121	IQIEMIKRELPAVSSDLKYTLRPTTVNSTSMVEVNPANRRDKQQTYNLTGLQPTTEYVI	180							
Db	172	IQIEMIKRELPAVSSDLKYTLRPTTVNSTSMVEVNPANRRDKQQTYNLTGLQPTTEYVI	231							
QY	181	ALRCAYVESKFSWSDMSQEKMGMTTEEAR	208							
Db	232	ALRCAYVESKFSWSDMSQEKMGMTTEEAR	259							

RESULT 6	
ABBS5002	
ID	ABBS5002 standard; Protein, 582 AA.
XX	
AC	ABBS5002;
XX	
DT	16-MAY-2002 (first entry)
XX	
DE	Human PRO21384 protein sequence SEQ ID NO:372.

KM Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
 KM vulnerability; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KM gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KM angiogenic disorder; cardiac hypertrophy; antiarteriosclerosis; hypertension;
 KM age-related macular degeneration; arterial restenosis; angina;
 KM rheumatoid arthritis; myocardial infarction; thrombophilic; angitis;
 KM lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KM wound healing; chromosome mapping; gene mapping.

OS	Homo sapiens.
XX	
PN	WO200200690-A2.

[illegible]

Query Match	100.0%	Score 1121	DB 23	Length 582
Best Local Similarity	100.0%	Pred. No. 6.2e-103		
Matches 208	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ALPAKAPENISCVYYRRKRLTCTWSPGKETSQYQVTKRYAFGEKXNDCTNTSSSTSENRA	60	
DB	52	ALPAPAPENISCVYYRRKRLTCTWSPGKETSQYQVTKRYAFGEKXNDCTNTSSSTSENRA	111	
QY	61	SCSFFLPITTPDNTTIEVEANGDGVIKSHMTYRLLENIAKTEBPPIFRVPVIGIKRM	120	
DB	112	SCSFFLPITTPDNTTIEVEANGDGVIKSHMTYRLLENIAKTEBPPIFRVPVIGIKRM	171	
QY	121	IQIETIKIKELAVSSDCKTTLAFRTVNSGSMWEVNPAPKRRKRNQTNLTGLOPTEEYI	180	
DB	172	IQIETIKIKELAVSSDCKTTLAFRTVNSGSMWEVNPAPKRRKRNQTNLTGLOPTEEYI	231	
QY	181	ALRCVAKESKFWSDMSOEKMGTEEEAP	208	
DB	232	ALRCVAKESKFWSDMSOEKMGTEEEAP	259	
RESULT 7				
ID	AAU83637			
	AAU83637	standard; Protein; 582 AA.		
AC	AAU83637			
XX				
DT	08-MAY-2002	(first entry)		
XX				
DE	Human PRO protein, Seq ID No 92.			
XX				
KM	Human; secreted protein; PRO; tumour; lung cancer; colon cancer;			

KM	breast cancer; prostate tumour; rectal tumour; liver tumour;
KW	papillary cell proliferation; chondrocyte cell proliferation;
KM	tumour necrosis factor-alpha.
XX	
OS	Homo sapiens.
XX	
PN	WO200208286-A2.
XX	
PD	31-JAN-2002.
PF	
PR	29-JUN-2001; 2001WO-US21066.
XX	
PR	20-JUL-2000; 2000US-219556P.
PR	25-JUL-2000; 2000US-220585P.
PR	25-JUL-2000; 2000US-220605P.
PR	25-JUL-2000; 2000US-220607P.
PR	25-JUL-2000; 2000US-220624P.
PR	25-JUL-2000; 2000US-220638P.
PR	25-JUL-2000; 2000US-220664P.
PR	25-JUL-2000; 2000US-220666P.
PR	26-JUL-2000; 2000US-220893P.
PR	28-JUL-2000; 2000WO-US20710.
PR	23-AUG-2000; 2000WO-US23522.
PR	24-AUG-2000; 2000WO-US23328.
PR	15-SEP-2000; 2000US-000000P.
PR	10-NOV-2000; 2000WO-US30873.
PR	28-NOV-2000; 2000US-253646P.
PR	01-DEC-2000; 2000WO-US32678.
PR	20-DEC-2000; 2000US-0747259.
PR	20-DEC-2000; 2000WO-US34956.
PR	28-FEB-2001; 2001WO-US06520.
PR	10-MAY-2001; 2001US-0854280.
XX	25-MAY-2001; 2001WO-US17092.
PA	(GETH) GENENTECH INC.
PI	Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI	Grimaldi JC, Gunney AL, Smith V, Stephan JF, Watanabe CK, Wood WT,
XX	
DR	N-PSDB; ABK33581.
XX	
PT	WP1; 2002-172001/22.
PT	
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT	useful for treating a PRO related disorder and for diagnosing tumours
PT	such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX	tumour or liver tumour -
BS	
CC	Claim 11; Figure 92; 359pp; English.
XX	
CC	The invention relates to one hundred and twenty two nucleic acids
CC	encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC	encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC	agonists and antagonists are useful for treating a PRO related disorder.
CC	The PRO polypeptides are useful for diagnosing tumours, especially lung
CC	cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC	liver tumour. The PRO polypeptides are useful for stimulating the
CC	proliferation of, or gene expression, in pericyte cells, for stimulating
CC	the proliferation or differentiation of chondrocyte cells, for
CC	stimulating the release of tumour necrosis factor-alpha from human blood,
CC	for stimulating or inhibiting the proliferation of normal human dermal
CC	fibroblast cells. The PRO polypeptide may also be used as molecular
CC	weight markers and for tissue typing. The PRO nucleic acids have
CC	applications in molecular biology, including use as hybridisation probes,
CC	and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC	protein sequences of the invention.
XX	
SO	Sequence 582 AA:
Query Match	100.0%; Score 1121; DB 23; Length 582;
Best Local Similarity	100.0%; Pred. No. 6, 2e-103;
Matches 208; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

1 ALPAKPENISCVYYRKNLCTGWSPGKETSYTYTKRYTAFGEKHNDCTNNSSTSENRA 60

Db 52 ALPAPEINISCVYYRKNLTCTWSPGKETSQYVYKRTYAFGEHNDCTNNSISEMRA 111
 Qy 61 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRLENIAKTEPPKIFRVKPVLGIKRM 120
 Db 112 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRLENIAKTEPPKIFRVKPVLGIKRM 171
 Qy 121 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVFAKNRDKNQYTNLTGLQPTETVI 180
 Db 172 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVFAKNRDKNQYTNLTGLQPTETVI 231
 Qy 181 ALRCVAKESKFWSDMSQEKMGTEBEAP 208
 Db 232 ALRCVAKESKFWSDMSQEKMGTEBEAP 259

RESULT 8

ABP54366 standard; Protein; 627 AA.

ID ABP54366 standard; Protein; 627 AA.
 AC ABP54366;
 DT 20-JAN-2003 (first entry)
 DE Human NR10.5 splicing variant protein SEQ ID NO:8.
 KW NR10; splicing variant; haematopoietic receptor; immunomodulator;
 KW haemostatic; haematopoietic factor; immunological disease;
 KW haematopoietic disease; haematopoietic cell regulation.
 OS Homo sapiens.
 PN WO200272730-A1.
 PD 03-OCT-2002.
 PF 22-MAR-2002; 2002WO-JP02769.
 PR 26-MAR-2001; 2001JP-0087298.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Maeda M, Yaguchi N, Hasegawa M;
 DR N-PSDB; ABQ83366.
 XX NR10 splicing variants of hematopoietic receptor proteins and encoded
 PT genes, applicable in searching hematopoietic factors and developing
 PT remedies for immunological and hematopoietic diseases
 PS Claim 1; Fig 10-12; 250pp; Japanese.
 CC The present invention describes haematopoietic receptor NR10 splicing
 CC variants (I). (I) have immunomodulator and haemostatic activities. The
 CC proteins and encoded genes are applicable in searching for novel
 CC haematopoietic factors, and developing remedies for immunological and
 CC haematopoietic diseases. The haematopoietic receptor genes participate
 CC in vivo immunomodulation and haematopoietic cell regulation, and in
 CC the search for haematopoietic factors capable of functionally binding
 CC to the receptors. The present sequence represents the human NR10.5
 CC protein from the present invention.
 SQ Sequence 627 AA;

Query Match 100.0%; Score 1121; DB 24; Length 627;
 Best Local Similarity 100.0%; Pred. No. 6.9e-103;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPAPEINISCVYYRKNLTCTWSPGKETSQYVYKRTYAFGEHNDCTNNSISEMRA 60
 Db 52 ALPAPEINISCVYYRKNLTCTWSPGKETSQYVYKRTYAFGEHNDCTNNSISEMRA 111

Qy 61 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRLENIAKTEPPKIFRVKPVLGIKRM 120
 Db 112 SCSEFLPRITIPDNNTIEVEANGDGVKSHMTYRLENIAKTEPPKIFRVKPVLGIKRM 171
 Qy 121 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVFAKNRDKNQYTNLTGLQPTETVI 180
 Db 172 IQIEWIKPELAPVSSDLKYTLRFRVTNSTSMWEVFAKNRDKNQYTNLTGLQPTETVI 231
 Qy 181 ALRCVAKESKFWSDMSQEKMGTEBEAP 208
 Db 232 ALRCVAKESKFWSDMSQEKMGTEBEAP 259

RESULT 9

ABB05738 standard; Protein; 649 AA.

ID ABB05738 standard; Protein; 649 AA.
 AC ABB05738;
 DT 01-MAY-2002 (first entry)
 DE Human zcytor17 protein sequence SEQ ID NO:46.
 KW Zcytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.
 OS Homo sapiens.
 PN WO20020721-A2.
 PD 03-JAN-2002.
 PF 26-JUN-2001; 2001WO-US20484.
 PR 26-JUN-2000; 2000US-214282P.
 PR 29-JUN-2000; 2000US-214955P.
 PR 08-FEB-2001; 2001US-267963P.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
 PI Maurer WF;
 DR N-PSDB; ABA93803.
 XX WPI; 2002-090519/12.
 PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders
 PS Claim 18; Page 195-197; 235pp; English.
 CC The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antirheumatic, antiviral, cytostatic,
 CC antineumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, such as in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukopenias. Antagonists of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the Sg11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention.

Sequence 649 AA;
Query Match 100.0%; Score 1121; DB 23; Length 649;
Best Local Similarity 100.0%; Pred. No. 7, 2e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSENRA 60
DB 20 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSENRA 79
QY 61 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYWRLENIAKTEPPKIFPVKVLGIKRM 120
DB 80 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYWRLENIAKTEPPKIFPVKVLGIKRM 139
QY 121 IOLEWIKPELAPVSSDLKYLFRFTVNSTSMWEVNFAPAKRDKNQYTNLTGLQPFTEYVI 180
DB 140 IOLEWIKPELAPVSSDLKYLFRFTVNSTSMWEVNFAPAKRDKNQYTNLTGLQPFTEYVI 199
QY 181 ALRCAYVESKFSWSDMSQEKMGTEEBAP 208
DB 200 ALRCAYVESKFSWSDMSQEKMGTEEBAP 227

RESULT 10

AB51242
ID AAB51242 standard; Protein; 652 AA.

AC AAB51242;

DT 26-MAR-2001 (first entry)

DE Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.

XX Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KM immunoregulation; haematopoietic cell regulation; transmembrane;
KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW metal allergy; pollen allergy.

XX Homo sapiens.

PN W02000425314-A1.

PD 14-DEC-2000.

PF 01-JUN-2000; 2000WO-JP03556.

PR 02-JUN-1999; 99JP-0155797.

PR 30-JUL-1999; 99JP-0217797.

PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Maeda M, Yaguchi N;

DR WPI; 2001-061720/07.

DR N-PSDB; AAC92337.

PT Hematopoietin receptor protein NR10 for screening potential ligands for
treatment of immune and haematopoietic disorders such as autoimmune
diseases and allergies -

PS Claim 1; Fig 3-5; 127pp; Japanese.

XX The present sequence represents a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell
CC regulation in vivo, and is useful in searching for haematopoietic
CC factors capable of binding to the receptor. NR10 can be used for the
CC identification of substances for the treatment and prevention of immune
CC and haematopoietic disorders including autoimmune diseases and allergies
CC such as metal and pollen allergy.

XX Sequence 652 AA;

Query Match 100.0%; Score 1121; DB 22; Length 652;
Best Local Similarity 100.0%; Pred. No. 7, 3e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSENRA 60
DB 33 ALPAKPNISCVYYRRKRLCTWSPGKETSYYQYVRYAFGEKDNCTNSSENRA 92
QY 61 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYWRLENIAKTEPPKIFPVKVLGIKRM 120
DB 93 SCSEFLPRITIPDNYTTEVAENGDDGVYKSHMTYWRLENIAKTEPPKIFPVKVLGIKRM 152
QY 121 IOLEWIKPELAPVSSDLKYLFRFTVNSTSMWEVNFAPAKRDKNQYTNLTGLQPFTEYVI 180
DB 153 IOLEWIKPELAPVSSDLKYLFRFTVNSTSMWEVNFAPAKRDKNQYTNLTGLQPFTEYVI 212
QY 181 ALRCAYVESKFSWSDMSQEKMGTEEBAP 208
DB 213 ALRCAYVESKFSWSDMSQEKMGTEEBAP 240

RESULT 11

AAE24028
ID AAB24028 standard; Protein; 652 AA.

AC AAE24028;

DT 23-SEP-2002 (first entry)

DE Human HPR1 variant protein #2.

XX Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
KM pancytopenia; leukopenia; anaemia; thrombocytopaenia; osteoporosis;
KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
KW osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;
KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
KW ischaemic disease; variant.

XX Homo sapiens.

PN W0200229060-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-US31634.

PR 06-OCT-2000; 2000US-238706P.

PR 13-OCT-2000; 2000US-240476P.

PR 20-FEB-2001; 2001US-270282P.

PA (IMNV) IMMUNEX CORP.

PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;

DR WPI; 2002-330172/36.

PT Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,
useful for treating cell proliferation, metabolic, and reproductive
hormone related conditions -

PS Disclosure; Page 110-112; 136pp; English.

XX The present invention relates to human and murine haematopoietin receptor
CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
CC anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis
CC resulting from a lack of bone-forming cells. They are also useful for

treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related conditions. They are useful for treating various haematologic and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelodysplastic syndromes (including refractory anaemia, refractory anaemia with ringed sideroblasts or with excess blasts), idiopathic thrombocytopenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/myeloid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, peridontitis resulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polyneuropathy, Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy, Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity, deficient mammary development and infertility. The present sequence is human HPR1 variant protein.

XX XX Sequence 652 AA;

Query Match 100.0%; Score 1121; DB 23; Length 652;

Best Local Similarity 100.0%; Pred. No. 7.3e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 60
DB 33 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 92
QY 61 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEBPXIFRYKPVLGIRK 120
DB 93 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEBPXIFRYKPVLGIRK 152
QY 121 IQIEWIKPELAPVSSDLKTYLRFRTVNSTSWMEVFAKNRDKKQNTYNLGLQPTTEYVI 180
DB 153 IQIEWIKPELAPVSSDLKTYLRFRTVNSTSWMEVFAKNRDKKQNTYNLGLQPTTEYVI 212
QY 181 ALRCVAKSKFWSDWSOEKMGTEBEAP 208
DB 213 ALRCVAKSKFWSDWSOEKMGTEBEAP 240

RESULT 12

AAB51244 ID AAB51244 standard; Protein; 662 AA.

XX AC AAB51244;

XX DT 26-MAR-2001 (first entry)

XX DE Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.

XX XX Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;

KW immunoregulation; haematopoietic cell regulation; transmembrane;

KM immune disorder; haematopoietic disorder; autoimmune disease; allergy;

XX KM metal allergy; pollen allergy.

OS Homo sapiens.

XX PN WO200075314-A1.

XX PD 14-DEC-2000.

XX PF 01-JUN-2000; 2000WO-JP03556.

XX PR 02-JUN-1999; 99JP-0155797.
XX PR 30-JUN-1999; 99JP-0217797.
XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PI Maeda M, Yaguchi N;
XX DR WPI; 2001-061720/07.
XX DR N-PSDB; AAC92350.

PT Hematopoietin receptor protein NR10 for screening potential ligands for treatment of immune and hematopoietic disorders such as autoimmune diseases and allergies -

XX PS Claim 1; Fig 13-14; 127pp; Japanese.

XX XX The present sequence represents a human haemopoietin receptor protein (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane protein and a soluble protein. NR10 is a haemopoietin receptor molecule which participates in immunoregulation and haematopoietic cell regulation in vivo, and is useful in searching for haematopoietic factors capable of binding to the receptor. NR10 can be used for the identification of substances for the treatment and prevention of immune and haematopoietic disorders including autoimmune diseases and allergies such as metal and pollen allergy.

XX XX Sequence 662 AA;

Query Match 100.0%; Score 1121; DB 22; Length 662;

Best Local Similarity 100.0%; Pred. No. 7.5e-103; Mismatches 0; Indels 0; Gaps 0;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 60
DB 33 ALPAKPNISCVYYRRKRLCTWSPGKETSQTQYTKRTAFGEKHNDCTNSTSENRA 92
QY 61 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEBPXIFRYKPVLGIRK 120
DB 93 SCSPFLPRITIPDNTTIEVAENGSGVYKSHMTYRLNIAKTEBPXIFRYKPVLGIRK 152
QY 121 IQIEWIKPELAPVSSDLKTYLRFRTVNSTSWMEVFAKNRDKKQNTYNLGLQPTTEYVI 180
DB 153 IQIEWIKPELAPVSSDLKTYLRFRTVNSTSWMEVFAKNRDKKQNTYNLGLQPTTEYVI 212
QY 181 ALRCVAKSKFWSDWSOEKMGTEBEAP 208
DB 213 ALRCVAKSKFWSDWSOEKMGTEBEAP 240

RESULT 13

AAE24029 ID AAE24029 standard; Protein; 662 AA.

XX AC AAE24029;

XX DT 23-SEP-2002 (first entry)

XX DE Human HPR1 variant protein #3.

XX XX Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;

KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;

KM neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;

KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;

KM ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;

KW osteoclast disorder; peridontitis; acute polyneuropathy; Bell's palsy;

KM anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;

KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;

KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;

KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;

KM ischaemic disease; variant.

OS Homo sapiens.

XX NO200229060-A2.
 PN 11-APR-2002.
 PD 05-OCT-2001; 2001WO-US31634.
 PF 06-OCT-2000; 2000US-238706P.
 PR 13-OCT-2000; 2000US-240476P.
 PR 20-FEB-2001; 2001US-270282P.
 XX (IMMV) IMMUNEX CORP.
 PA Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
 PI WPI; 2002-330172/36.
 DR Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions -
 PS Disclosure; Page 112-115; 136pp; English.
 XX The present invention relates to human and murine hematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukaemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various hematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), hematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC masthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence
 CC is human HPR1 variant protein.
 XX
 SQ Sequence 662 AA;
 Query Match 100.0%; Score 1121; DB 23; Length 662;
 Best Local Similarity 100.0%; Pred. No. 7, 5e-103;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALPAKPNISCVYYRKNLCTWSPGKETSYYQYTVKRYAFGEKHDNCTNSTSENRA 60
 DB 33 ALPAKPNISCVYYRKNLCTWSPGKETSYYQYTVKRYAFGEKHDNCTNSTSENRA 92
 QY 61 SCSEFLFRITTPDNTTIEVAENGQVYKSHMTYWRLENTAKTEPKIFRYKPYLGIKRM 120
 DB 93 SCSEFLFRITTPDNTTIEVAENGQVYKSHMTYWRLENTAKTEPKIFRYKPYLGIKRM 152
 QY 121 IOIEWIKPELAPVSSDKYTLRFPTUNSTSMENYFNPAKRNKQKQNTNLTGLQPFITYVI 180
 DB 153 IOIEWIKPELAPVSSDKYTLRFPTUNSTSMENYFNPAKRNKQKQNTNLTGLQPFITYVI 212

QY 181 ALRCAYESKFWSDWSQEKMGTEEBAP 208
 DB 213 ALRCAYESKFWSDWSQEKMGTEEBAP 240
 RESULT 14
 ABB05741
 ID ABB05741 standard; Protein; 662 AA.
 XX
 AC ABB05741;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human zcytor17 protein sequence SEQ ID NO:54.
 XX
 KW Zcytor17, chromosome 5; 5q11, cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antineuronic; antiarthritic; cyostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200200721-A2.
 XX
 PD 03-JUN-2002.
 XX
 XX 26-JUN-2001; 2001WO-US20484.
 XX
 XX 26-JUN-2000; 2000US-214282P.
 PR 29-JUN-2000; 2000US-214955P.
 PR 08-FEB-2001; 2001US-267963P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuiper JL;
 PI Maurer ME;
 DR WPI; 2002-090519/12.
 DR N-PSDB; ABA93808.
 DR
 XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders -
 PS Example 1; Page 204-206; 235pp; English.
 XX
 PS The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cyostatic,
 CC antineuronic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, such as in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 662 AA;
 Query Match 100.0%; Score 1121; DB 23; Length 662;
 Best Local Similarity 100.0%; Pred. No. 7, 5e-103;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ALPAKPNISCVYYRKNLCTWSPGKETSYYQYTVKRYAFGEKHDNCTNSTSENRA 60

Db 33 ALPAKPNISCVYYRRKVLCTWSPGKETSQTQVTKRTYAFGEKHDNCTNNSSTSENRA 92
QY 61 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYWRLENIakteppkIFRVKVLGIKRM 120
Db 93 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYWRLENIakteppkIFRVKVLGIKRM 152
QY 121 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRDKDKQTYNLTLGLQPFTEYVI 180
Db 153 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRDKDKQTYNLTLGLQPFTEYVI 212
QY 181 ALRCAVSKSKFWSQKMGMTBEAP 208
Db 213 ALRCAVSKSKFWSQKMGMTBEAP 240

RESULT 15
ABP54363
ID ABP54363 standard; Protein; 681 AA.

XX AC ABP54363;

DT 20-JAN-2003 (first entry)

DE Human NR10.3 splicing variant protein SEQ ID NO:2.

XX NR10; splicing variant; haematopoietic receptor; immunomodulator;

KM haemostatic; haematopoietic factor; immunological disease;

KM haematopoietic disease; haematopoietic cell regulation.

XX Homo sapiens.

PN WO20027230-A1.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

DR WPI; 2003-018925/01.

DR N-PSDB; ABQ83363.

PT NR10 splicing variants of hematopoietic receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -

XX Example 2; Fig 3; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietic receptor genes participate
CC in in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.3
CC protein from the present invention.

XX Sequence 681 AA;

Query Match 100.0%; Score 1121; DB 24; Length 681;

Best Local Similarity 100.0%; Pred. No. 7.8e-103;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKVLCTWSPGKETSQTQVTKRTYAFGEKHDNCTNNSSTSENRA 60
Db 52 ALPAKPNISCVYYRRKVLCTWSPGKETSQTQVTKRTYAFGEKHDNCTNNSSTSENRA 111

QY 61 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYWRLENIakteppkIFRVKVLGIKRM 120
Db 112 SCSEFLPRITIPDNYTIEVEAENGDVYKSHMTYWRLENIakteppkIFRVKVLGIKRM 171
QY 121 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRDKDKQTYNLTLGLQPFTEYVI 180
Db 172 IOIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFANRDKDKQTYNLTLGLQPFTEYVI 231
QY 181 ALRCAVSKSKFWSQKMGMTBEAP 208
Db 232 ALRCAVSKSKFWSQKMGMTBEAP 259

Search completed: August 18, 2003, 13:27:00
Job time : 80.0499 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2003, 13:24:23 ; Search time 25.6912 Seconds
(without alignments)
342.555 Million cell updates/sec

Title: US-09-892-949-2_COPY_20_227

Perfect score: 1121

Sequence: 1 ALPAPENISCVYRKNLT.....SKFWSQSKMGTEBEAP 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A-COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B-COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A-COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B-COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCTUS-COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	268.5	24.0	332	4 US-09-313-942-10	Sequence 10, App1
2	268.5	24.0	488	2 US-08-539-455B-5	Sequence 5, App1
3	268.5	24.0	488	3 US-09-069-781B-5	Sequence 5, App1
4	268.5	24.0	488	4 US-09-137-132-5	Sequence 5, App1
5	268.5	24.0	488	4 US-08-864-564A-5	Sequence 5, App1
6	268.5	24.0	488	4 US-09-094-410-5	Sequence 5, App1
7	268.5	24.0	488	4 US-08-708-123D-5	Sequence 5, App1
8	268.5	24.0	488	4 US-08-583-153A-5	Sequence 5, App1
9	268.5	24.0	488	4 US-08-638-524B-5	Sequence 5, App1
10	268.5	24.0	658	2 US-08-825-558-4	Sequence 4, App1
11	268.5	24.0	658	4 US-07-312-611-4	Sequence 4, App1
12	268.5	24.0	708	1 US-07-797-556-2	Sequence 2, App1
13	268.5	24.0	708	1 US-08-308-881-2	Sequence 2, App1
14	268.5	24.0	708	2 US-09-058-263-2	Sequence 2, App1
15	268.5	24.0	708	2 US-09-059-099-2	Sequence 2, App1
16	268.5	24.0	708	3 US-09-058-264-2	Sequence 2, App1
17	268.5	24.0	708	4 US-09-455-962-2	Sequence 2, App1
18	268.5	24.0	708	5 PCT-US95-06530-2	Sequence 2, App1
19	268.5	24.0	859	4 US-09-313-942-7	Sequence 7, App1
20	268.5	24.0	918	2 US-08-825-558-6	Sequence 6, App1
21	268.5	24.0	918	4 US-09-312-611-6	Sequence 6, App1
22	268.5	24.0	918	4 US-09-313-942-9	Sequence 9, App1
23	268.5	24.0	1158	4 US-09-313-942-26	Sequence 26, App1
24	268.5	24.0	1158	4 US-09-313-942-24	Sequence 24, App1
25	235	21.0	389	3 US-09-071-224-26	Sequence 26, App1
26	232	20.7	389	3 US-09-071-224-24	Sequence 24, App1
27	232	20.7	389	3 US-09-071-224-29	Sequence 29, App1

28	231	20.6	385	3 US-09-071-224-20	Sequence 20, App1
29	231	20.6	388	3 US-09-071-224-17	Sequence 17, App1
30	231	20.6	389	3 US-09-071-224-22	Sequence 22, App1
31	231	20.6	389	3 US-09-071-224-25	Sequence 25, App1
32	231	20.6	392	3 US-09-071-224-18	Sequence 18, App1
33	231	20.6	422	3 US-09-071-224-2	Sequence 2, App1
34	231	20.6	425	3 US-09-071-224-4	Sequence 4, App1
35	230.5	20.6	303	3 US-09-071-224-21	Sequence 21, App1
36	230.5	20.6	303	3 US-09-071-224-23	Sequence 23, App1
37	230	20.5	389	3 US-09-071-224-27	Sequence 27, App1
38	230	20.5	389	3 US-09-071-224-28	Sequence 28, App1
39	229	20.5	389	3 US-09-071-224-31	Sequence 31, App1
40	229	20.4	385	3 US-09-071-224-19	Sequence 19, App1
41	229	20.4	389	3 US-09-071-224-30	Sequence 30, App1
42	229	20.4	405	3 US-09-012-072-2	Sequence 2, App1
43	229	20.4	405	3 US-09-120-601-2	Sequence 2, App1
44	229	20.4	425	3 US-09-071-224-6	Sequence 6, App1
45	214	19.1	572	2 US-08-419-652-5	Sequence 5, App1

ALIGNMENTS

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RESULT 1
US-09-313-942-10
; Sequence 10, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-10
Query Match 24.0%, Score 268.5, DB 4, Length 332;
Best Local Similarity 30.3%, Pred. No. 3.3e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;
QY 3 PAKENISCVYRKNLTCTWSPGKETS-TQTVK---RTYAFGB---KHD---NCTTN 52
DB 126 PEKPKLSCITVNEGKKRCMDGGRTHLETFILSEWAIHFAQCKARDPISCTVD 185
QY 53 SSTSENRAASCPELPITIPDNYTTEVEAENGGVKIS-HMTYWRLENIATKEPPKIFRY 111
DB 186 YSP-----VFV-----NIEVWEAENLKGKTSQSHINFPYVK-KRPENLSEV 230
QY 112 KPYLGKIKMIQIEWIKPELAPVSSDIKYLRFRTVNSTGSMVEVFAKNRKNQYNTLNG 171
DB 231 INSEELSSIKIKLWTNPSIKSVI-LKYNIOYRTKDSATWSQIP-DEDTASTRSPTVOD 288
QY 172 LQFTEYVIALRCVAKESK-FWSQSKMGTEBEAP 208
DB 289 LKPFTEYVRIRKMDGKGWSDSEBSAGLTEDRP 326
RESULT 2
US-08-599-455B-5
; Sequence 5, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartag11a, Louis A.
```

APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-599-455B-5

Query Match 24.0%; Score 268.5; DB 2; Length 488;
Best Local Similarity 30.3%; Pred. No. 5.7e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKNLITCWSPGKETS-TOYTVK---RTVAFGE---KHD---NCTTN 52
Db 97 PEKRNLSCTIVNKGKRCMDGSGRETHLETNFTLKSMAWTHKADCAKADPTSTCTVD 156.
QY 53 SSTSENRA SCFPLPRITIPDNYTIEVAENGGVKIS-HMTYWRLENIATPEPKIFRV 111
Db 157 YST-----YFV-----NIEWWEAENALGKVTSDHINPDYKVV-KPNPPhNLsv 201
QY 112 KPVLGIRKMIQIEMIKPELAPVSSDLKTLRFRVNSTGSMWEVNFAPKRRKDKQNTYNLTG 171
Db 202 INSEELSSILKLTWTNPSIKSVII-LKYNIQYRTKASTWSQIP-PEDTASTRSSFTVOD 259
QY 172 LQPFTEYVIALRCVAKESK-FMSDMSORHGMTEEAR 208
Db 260 LKPFTEYVIRICMEKDGKGYSDMSEASGIYYEDRP 297

RESULT 3
US-09-069-781B-5
Sequence 5, Application US/09069781B
Patent No. 6287782
GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,781B
FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: US 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-069-781B-5

Query Match 24.0%; Score 268.5; DB 3; Length 488;
Best Local Similarity 30.3%; Pred. No. 5.7e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKNLITCWSPGKETS-TOYTVK---RTVAFGE---KHD---NCTTN 52
Db 97 PEKRNLSCTIVNKGKRCMDGSGRETHLETNFTLKSMAWTHKADCAKADPTSTCTVD 156
QY 53 SSTSENRA SCFPLPRITIPDNYTIEVAENGGVKIS-HMTYWRLENIATPEPKIFRV 111
Db 157 YST-----YFV-----NIEWWEAENALGKVTSDHINPDYKVV-KPNPPhNLsv 201
QY 112 KPVLGIRKMIQIEMIKPELAPVSSDLKTLRFRVNSTGSMWEVNFAPKRRKDKQNTYNLTG 171
Db 202 INSEELSSILKLTWTNPSIKSVII-LKYNIQYRTKASTWSQIP-PEDTASTRSSFTVOD 259

Qy 172 LQPTFVYIALRCVAKESK-FWSDWSQKMGTEEBAP 208
Db 260 LKPFTEYVIRICMKEDGKGYSDWSEBASGITVEDRP 297

RESULT 4

US-09-137-132-5
Sequence 5, Application US/09137132
Patent No. 6380363
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE OB RECEPTOR AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,132
FILING DATE: 18-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-137-132-5

Query Match 24.0%; Score 268.5; DB 4; Length 488;
Best Local Similarity 30.3%; Pred. No. 5.7e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

Qy 3 PAKPENICVYYRRNLCTSPKETS-YQYTK---RTYAGE---KHD---NCTTN 52
Db 97 PEKPNLSCIIVVEGKRCCEMDGGRHLETNFTLKSWMATHKFPADCKAKDPTPTCTVD 156
Qy 53 SGTSENKASCSFELRIRIIPNYTIEVEANDGVYKS-HNTYMWLENIATKEPKIRY 111
Db 157 YST-----YFV-----NIEVVEAENALGKVTSDHINFDVYRV-KENPHNLISV 201
Qy 112 KVLGKEMIQLEWIKPELAPVSDLYTLRFRYVNSTSWMEVNFARKKDKQNTYNLTG 171
Db 202 INSELSLTKLTWNPISIKSVII-LKYNIQRTDASTWQIR-PEDTASTRSSFTYQD 259

Qy 172 LQPTFVYIALRCVAKESK-FWSDWSQKMGTEEBAP 208
Db 260 LKPFTEYVIRICMKEDGKGYSDWSEBASGITVEDRP 297

RESULT 5

US-08-864-564A-5
Sequence 5, Application US/08864564A
Patent No. 6395498
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE OB RECEPTOR AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,564A
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/708,123
FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/638,524
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids

TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-864-564A-5

Query Match 24.0%; Score 268.5; DB 4; Length 488;
Best Local Similarity 30.3%; Pred. No. 5,7e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKULCTWSPGKESY--TOYTK---RTYAFGE---KHD---NCTTN 52
DB 97 PEKPNLSCTIVNEGKRCMDGGRTHLETFTLSEWATHKFADCKARDPPTSCTVD 156
QY 53 SSTSENRA SCSPFLPRITIPDNYTIEVEANGDVYKS-HMTYWRLENI AKTEPPKIFRY 111
DB 157 YST-----VYFV-----NIEVWEAENALGKVTSDHINDPYKVK-KPNPNNLSV 201
QY 112 KPVLGIRKMIQIEMIKELAPVSSDLKTLRPTVNSTSWMEVNFANRKKQTYNLG 171
DB 202 INSEELSSILKLTWNPISIKSVII-LKYNIOYRTKDSWTSQIP-PEDTASTRSSPTVOD 259
QY 172 LOPTEYVIALRCAYESK-FMSDMSOEKGMTEEPAP 208
DB 260 LKPFTEYVRIRCKEDGKGYSDMSSEASGITYEDRP 297

RESULT 6

US-09-094-410-5
Sequence 5, Application US/09094410
Patent No. 6403552

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/094,410

FILING DATE: 09-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/864,564

FILING DATE: 28-MAY-1997

APPLICATION NUMBER: 08/708,123

FILING DATE: 03-SEP-1996

APPLICATION NUMBER: 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

APPLICATION NUMBER: 08/570,142

FILING DATE: 11-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995

APPLICATION NUMBER: 08/566,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/562,663

ATTORNEY/AGENT INFORMATION:
NAME: Melkielejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 488 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

Query Match 24.0%; Score 268.5; DB 4; Length 488;
Best Local Similarity 30.3%; Pred. No. 5,7e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKULCTWSPGKESY--TOYTK---RTYAFGE---KHD---NCTTN 52
DB 97 PEKPNLSCTIVNEGKRCMDGGRTHLETFTLSEWATHKFADCKARDPPTSCTVD 156
QY 53 SSTSENRA SCSPFLPRITIPDNYTIEVEANGDVYKS-HMTYWRLENI AKTEPPKIFRY 111
DB 157 YST-----VYFV-----NIEVWEAENALGKVTSDHINDPYKVK-KPNPNNLSV 201
QY 112 KPVLGIRKMIQIEMIKELAPVSSDLKTLRPTVNSTSWMEVNFANRKKQTYNLG 171
DB 202 INSEELSSILKLTWNPISIKSVII-LKYNIOYRTKDSWTSQIP-PEDTASTRSSPTVOD 259
QY 172 LOPTEYVIALRCAYESK-FMSDMSOEKGMTEEPAP 208
DB 260 LKPFTEYVRIRCKEDGKGYSDMSSEASGITYEDRP 297

RESULT 7

US-08-708-123D-5
Sequence 5, Application US/08708123D
Patent No. 6482927

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tepper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: White, David W.

TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR

TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/708,123D

FILING DATE: 03-SEP-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/638,524

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/583,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/570,142

RESULT 10
 US-08-825-558-4
 Sequence 4, Application US/08825558
 Patent No. 5865724
 GENERAL INFORMATION:
 APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 APPLICANT: DELLOW, KIMBERLEY A.
 TITLE OF INVENTION: Gp 130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/825,558

RESULT 11
 US-09-312-611-4
 Sequence 4, Application US/09312611
 Patent No. 6380160
 GENERAL INFORMATION:
 APPLICANT: SHARKEY, ANDREW
 APPLICANT: SMITH, STEPHEN K.
 APPLICANT: DELLOW, KIMBERLEY A.
 TITLE OF INVENTION: Gp130 Lacking the Transmembrane Domain
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
 STREET: 1100 NEW YORK AVENUE
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/312,611
 FILING DATE: 17-MAY-1999
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: ESMOND, ROBERT W.
 REGISTRATION NUMBER: 32, 893
 REFERENCE/DOCKET NUMBER: 0623_0530002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2500
 TELEFAX: (202)371-2540
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:

LENGTH: 658 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-312-611-4

Query Match 24.0%; Score 268.5; DB 4; Length 658;
Best Local Similarity 30.3%; Pred. No. 8.8e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKRLTCTWSPGKTSY-TQYTVK---RTYAFGE---KHD---NCTTN 52
DB 126 PEKPKRLSCIVNKGKRCMDGGRTHLETNFTLKSEWATHKFAACKAKRDTPTSCYVD 185
QY 53 SSTESENABSCSFFLPRTIPDNVTIEVEANGDGVKS-HMTYWRLENIAKTEPPKIFRY 111
DB 186 YST-----VYFV-----NIEVWEAENALGKVTSDHINFDYKVK-KENPPHNLISV 230
QY 112 KPVLGIRMIQIEMIKPELAPVSSDKYTLRFTVNSTGMEVNFANRKNQYTNLNG 171
DB 231 INSEELSLIKLTWNPISIKSVII-LKYNIQRTDASTWSQIP-PEDTASTRSSFTYVD 288
QY 172 LQPFTEYVIALRCAYESK-FMSDMSQEKMGTEEBAP 208
DB 289 LKPFTEYVFRIRCMKEDGKGYMSWSEASGITVEDRP 326

RESULT 12

US-07-797-556-2
Sequence 2, Application US/07797556
Patent No. 5262522

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
TITLE OF INVENTION: Receptor for Oncostatin M and Leukemia
TITLE OF INVENTION: Inhibitory Factor
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/797,556
FILING DATE: 19911122
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2607
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
TELEFAX: 206-587-0606
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-797-556-2

Query Match 24.0%; Score 268.5; DB 1; Length 708;
Best Local Similarity 30.3%; Pred. No. 9.8e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;
QY 3 PAKPENISCVYYRRKRLTCTWSPGKTSY-TQYTVK---RTYAFGE---KHD---NCTTN 52
DB 126 PEKPKRLSCIVNKGKRCMDGGRTHLETNFTLKSEWATHKFAACKAKRDTPTSCYVD 185
QY 53 SSTESENABSCSFFLPRTIPDNVTIEVEANGDGVKS-HMTYWRLENIAKTEPPKIFRY 111
DB 186 YST-----VYFV-----NIEVWEAENALGKVTSDHINFDYKVK-KENPPHNLISV 230
QY 112 KPVLGIRMIQIEMIKPELAPVSSDKYTLRFTVNSTGMEVNFANRKNQYTNLNG 171
DB 231 INSEELSLIKLTWNPISIKSVII-LKYNIQRTDASTWSQIP-PEDTASTRSSFTYVD 288
QY 172 LQPFTEYVIALRCAYESK-FMSDMSQEKMGTEEBAP 208
DB 289 LKPFTEYVFRIRCMKEDGKGYMSWSEASGITVEDRP 326

DB 126 PEKPKRLSCIVNKGKRCMDGGRTHLETNFTLKSEWATHKFAACKAKRDTPTSCYVD 185
QY 53 SSTESENABSCSFFLPRTIPDNVTIEVEANGDGVKS-HMTYWRLENIAKTEPPKIFRY 111
DB 186 YST-----VYFV-----NIEVWEAENALGKVTSDHINFDYKVK-KENPPHNLISV 230

QY 112 KPVLGIRMIQIEMIKPELAPVSSDKYTLRFTVNSTGMEVNFANRKNQYTNLNG 171
DB 231 INSEELSLIKLTWNPISIKSVII-LKYNIQRTDASTWSQIP-PEDTASTRSSFTYVD 288

QY 172 LQPFTEYVIALRCAYESK-FMSDMSQEKMGTEEBAP 208
DB 289 LKPFTEYVFRIRCMKEDGKGYMSWSEASGITVEDRP 326

RESULT 13

US-08-308-881-2
Sequence 2, Application US/08308881
Patent No. 5783672

GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,881
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-308-881-2

Query Match 24.0%; Score 268.5; DB 1; Length 708;
Best Local Similarity 30.3%; Pred. No. 9.8e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYYRRKRLTCTWSPGKTSY-TQYTVK---RTYAFGE---KHD---NCTTN 52
DB 126 PEKPKRLSCIVNKGKRCMDGGRTHLETNFTLKSEWATHKFAACKAKRDTPTSCYVD 185
QY 53 SSTESENABSCSFFLPRTIPDNVTIEVEANGDGVKS-HMTYWRLENIAKTEPPKIFRY 111
DB 186 YST-----VYFV-----NIEVWEAENALGKVTSDHINFDYKVK-KENPPHNLISV 230
QY 112 KPVLGIRMIQIEMIKPELAPVSSDKYTLRFTVNSTGMEVNFANRKNQYTNLNG 171
DB 231 INSEELSLIKLTWNPISIKSVII-LKYNIQRTDASTWSQIP-PEDTASTRSSFTYVD 288
QY 172 LQPFTEYVIALRCAYESK-FMSDMSQEKMGTEEBAP 208
DB 289 LKPFTEYVFRIRCMKEDGKGYMSWSEASGITVEDRP 326

Db 231 INSEELSLIKLWTWNPISKVIIL-KYNIQYRTKQASTWSQIP-PEDTASTRSSFTVQD 288
QY 172 LQPFTEYVIALRCAYKESK-FWSDMSQEKMGMTSEAP 208
Db 289 LKPFTEYVIRIRCKMEDGKGWSDMSBBSAGITYEDRP 326

RESULT 14

US-09-058-263-2
Sequence 2, Application US/09058263
Patent No. 5891997
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,263
FILING DATE:
CLASSIFICATION:
Prior Application Number: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-058-263-2
Query Match 24.0%; Score 268.5; DB 2; Length 708;
Best Local Similarity 30.3%; Pred. No. 9.8e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;
QY 3 PAKPENISCVYIRKRLCTWSPGKETSY-TOYTVK---RTYAFGE---KHD---NCTTN 52
Db 126 PEKPKNLSCIVNKGKRCCEWGDGREGTHLETNFTLSEWATKRFADCKAKRDPPTSCVTD 185
QY 53 SSTSENBRASCSEFLPRITIPDNYTIEVEAENGQVYKS-HMTYWRLENIATKEPPKIFRY 111
Db 186 YST-----VYFV-----NIEWVEAENALGKVTSDHINDPYKY-KNPFNHLSV 230
QY 112 KPVLGIRKMIQIEWIKPELAPVSSDKYTLRFRYVNSTSMVEVNAKRNKQNTYNLTG 171
Db 231 INSEELSLIKLWTWNPISKVIIL-KYNIQYRTKQASTWSQIP-PEDTASTRSSFTVQD 288
QY 172 LQPFTEYVIALRCAYKESK-FWSDMSQEKMGMTSEAP 208
Db 289 LKPFTEYVIRIRCKMEDGKGWSDMSBBSAGITYEDRP 326

RESULT 15

US-09-059-099-2
Sequence 2, Application US/09059099
Patent No. 5925740
GENERAL INFORMATION:
APPLICANT: Mosley, Bruce
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Receptor for Oncostatin M
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,099
FILING DATE:
CLASSIFICATION:
Prior Application Number: US/08/308,881
FILING DATE: 12-SEP-1994
APPLICATION NUMBER: US 08/249,553
FILING DATE: 26-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2614-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-099-2

Query Match 24.0%; Score 268.5; DB 2; Length 708;
Best Local Similarity 30.3%; Pred. No. 9.8e-21;
Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;

QY 3 PAKPENISCVYIRKRLCTWSPGKETSY-TOYTVK---RTYAFGE---KHD---NCTTN 52
Db 126 PEKPKNLSCIVNKGKRCCEWGDGREGTHLETNFTLSEWATKRFADCKAKRDPPTSCVTD 185
QY 53 SSTSENBRASCSEFLPRITIPDNYTIEVEAENGQVYKS-HMTYWRLENIATKEPPKIFRY 111
Db 186 YST-----VYFV-----NIEWVEAENALGKVTSDHINDPYKY-KNPFNHLSV 230
QY 112 KPVLGIRKMIQIEWIKPELAPVSSDKYTLRFRYVNSTSMVEVNAKRNKQNTYNLTG 171
Db 231 INSEELSLIKLWTWNPISKVIIL-KYNIQYRTKQASTWSQIP-PEDTASTRSSFTVQD 288
QY 172 LQPFTEYVIALRCAYKESK-FWSDMSQEKMGMTSEAP 208
Db 289 LKPFTEYVIRIRCKMEDGKGWSDMSBBSAGITYEDRP 326

Search completed: August 18, 2003, 13:32:20
JOD time : 26.6912 secs

Mon Aug 18 14:06:52 2003

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:27:13 ; Search time 27.1734 Seconds
(without alignments)
1002.770 Million cell updates/sec

Title: US-09-892-949-2_COPY_20_227

Perfect score: 1121
Sequence: 1 ALPAKPNISCVYRKXNL.....SKFWSDSQKMKMTSEAP 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 492763 seqs, 131003257 residues

Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1121	100.0	582	12 US-10-216-163-92	Sequence 92, Appl
3	1121	100.0	582	15 US-10-227-884-92	Sequence 92, Appl
4	1121	100.0	582	15 US-10-230-163-92	Sequence 92, Appl
5	1121	100.0	582	15 US-10-230-338-92	Sequence 92, Appl
6	1121	100.0	582	15 US-10-230-631-92	Sequence 92, Appl
7	1121	100.0	582	15 US-10-230-414-92	Sequence 92, Appl
8	1121	100.0	582	15 US-10-216-1159A-92	Sequence 92, Appl
9	1121	100.0	582	15 US-10-218-849-92	Sequence 92, Appl
10	1121	100.0	582	15 US-10-227-873-92	Sequence 92, Appl
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32	1121	100.0	582	15 US-10-219-524-92	Sequence 92, Appl
33	1121	100.0	582	15 US-10-219-528-92	Sequence 92, Appl
34	1121	100.0	582	15 US-10-227-880-92	Sequence 92, Appl
35	1121	100.0	582	15 US-10-227-881-92	Sequence 92, Appl
36	1121	100.0	582	15 US-10-227-882-92	Sequence 92, Appl
37	1121	100.0	582	15 US-10-230-436-92	Sequence 92, Appl
38	1121	100.0	582	15 US-10-232-223-92	Sequence 92, Appl
39	1121	100.0	582	15 US-10-232-225-92	Sequence 92, Appl
40	1121	100.0	582	15 US-10-232-227-92	Sequence 92, Appl
41	1121	100.0	582	15 US-10-232-229-92	Sequence 92, Appl
42	1121	100.0	582	15 US-10-232-234-92	Sequence 92, Appl
43	1121	100.0	582	15 US-10-219-060-92	Sequence 92, Appl
44	1121	100.0	582	15 US-10-223-085-372	Sequence 92, Appl
45	1121	100.0	582	15 US-10-216-160-92	Sequence 92, Appl

ALIGNMENTS

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RESULT 1
US-09-892-949-18
; Sequence 18, Application US/09892949
; Publication No. US20030096339A1
GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Premeil, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-18
Query Match      100.0%; Score 1121; DB 11; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.1e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ALPAKPNISCVYRKXNLCTWSPKSTSYQYVTKTVAAGKNDCTNNTSSSENA 60
      20 ALPAKPNISCVYRKXNLCTWSPKSTSYQYVTKTVAAGKNDCTNNTSSSENA 79
QY      61 SCSFLLPRTITPDNTTIEVEAENGDVVKSHTWTWRLNIAKTEPPKIFRVKPVVGIKRM 120

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Db 80 SCSPFLPRITIPONTYITBEVAENGOSVISHMTYRLLENIAKTEBPKIFRFXPLGIKM 139
Qy 121 IOIEWIKPELAPVSDUKTTLRFRTYVNSTSMWEVPAKRRKDKONTYNLJGLPFEYVI 180
Db 140 IOIEWIKPELAPVSDUKTTLRFRTYVNSTSMWEVPAKRRKDKONTYNLJGLPFEYVI 199
Qy 181 ALRCAYVESKFWSMDSOEKMGMTTEBP 208
Db 200 ALRCAYVESKFWSMDSOEKMGMTTEBP 227

RESULT 2

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US-10-216-163-92
: Sequence 92, Application US/10216163
: Publication No. US20030149239A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Desnoyers, Luc
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Smith, Victoria
: APPLICANT: Stephan, Jean-Philippe F.
: APPLICANT: Watanabe, Colin L.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3530P1C3
: CURRENT APPLICATION NUMBER: US/10/216,163
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: 10/119,480
: PRIOR FILING DATE: 2002-04-09
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/062287
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063549
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/064103
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/066873
: PRIOR FILING DATE: 1997-12-17
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/079294
: PRIOR FILING DATE: 1998-03-25
: PRIOR APPLICATION NUMBER: 60/079656
: PRIOR FILING DATE: 1998-03-26
: PRIOR APPLICATION NUMBER: 60/079728
: PRIOR FILING DATE: 1998-03-27
: Remaining Prior Application data removed - See file Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 246
: SEQ ID NO 92
: LENGTH: 582
: TYPE: PRT
: ORGANISM: Homo Sapien
: US-10-216-163-92

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Query Match	100.0%;	Score 1121;	DB 12;	Length 582;
Best Local Similarity	100.0%;	Pred. No. 4.6e-104;		
Matches 208;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	ALAPKENISCVYYHKKNLCTWSPKESYYQYVKKTYAFGEHDCNTNNSSENRA	60
Db	ALAPKENISCVYYHKKNLCTWSPKESYYQYVKKTYAFGEHDCNTNNSSENRA	111
Qy	SCSFPFLRITIPNTTIEVAENGQVKSHTTWRLENIAKTEPPIFRVYPLVGIKRM	120
Db	SCSFPFLRITIPNTTIEVAENGQVKSHTTWRLENIAKTEPPIFRVYPLVGIKRM	171

Qy	121	10EWIKPELPAPSSDLKTTLRFRVNSTSMMEVNPAPNRKDKQVTNLGLQPFTEYVI	180
Db	172	IQEWIKPELPAPSSDLKTTLRFRVNSTSMMEVNPAPNRKDKQVTNLGLQDPFTEYVI	221
Qy	181	ALFCAVKESEKPFSDMSQERMGTEEEAP	208
Db	232	ALFCAVKESEKPFSDMSQERMGTEEEAP	259

RESULT 3

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1 Sequence 92, Application US/10227884
2 Publication No. US20030027988A1
3 GENERAL INFORMATION:
4 APPLICANT: Baker, Kevin P.
5 APPLICANT: Desnoyers, Luc
6 APPLICANT: Gerritsen, Mary
7 APPLICANT: Goddard, Audrey
8 APPLICANT: Godowski, Paul J.
9 APPLICANT: Grimaldi, J. Christopher
10 APPLICANT: Gurney, Austin L.
11 APPLICANT: Smith, Victoria
12 APPLICANT: Stephan, Jean-Philippe F.
13 APPLICANT: Matanabe, Colin L.
14 APPLICANT: Wood, William I.
15 TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
16 FILE REFERENCE: P9530P1C79
17 CURRENT APPLICATION NUMBER: US/10/227,884
18 PRIOR FILING DATE: 2002-08-26
19 PRIOR APPLICATION NUMBER: 10/119,480
20 PRIOR FILING DATE: 2002-04-09
21 PRIOR APPLICATION NUMBER: 60/059113
22 PRIOR FILING DATE: 1997-09-17
23 PRIOR APPLICATION NUMBER: 60/062287
24 PRIOR FILING DATE: 1997-10-17
25 PRIOR APPLICATION NUMBER: 60/063549
26 PRIOR FILING DATE: 1997-10-28
27 PRIOR APPLICATION NUMBER: 60/064103
28 PRIOR FILING DATE: 1997-10-31
29 PRIOR APPLICATION NUMBER: 60/069873
30 PRIOR FILING DATE: 1997-12-17
31 PRIOR APPLICATION NUMBER: 60/078910
32 PRIOR FILING DATE: 1998-03-20
33 PRIOR APPLICATION NUMBER: 60/079294
34 PRIOR FILING DATE: 1998-03-25
35 PRIOR APPLICATION NUMBER: 60/079656
36 PRIOR FILING DATE: 1998-03-26
37 PRIOR APPLICATION NUMBER: 60/079728
38 PRIOR FILING DATE: 1998-03-27
39 PRIOR APPLICATION NUMBER: 60/081819
40 PRIOR FILING DATE: 1998-04-15
41 PRIOR APPLICATION NUMBER: 60/081955
42 PRIOR FILING DATE: 1998-04-15
43 PRIOR APPLICATION NUMBER: 60/082804
44 PRIOR FILING DATE: 1998-04-22
45 PRIOR APPLICATION NUMBER: 60/084441
46 PRIOR FILING DATE: 1998-05-06
47 PRIOR APPLICATION NUMBER: 60/085323
48 PRIOR FILING DATE: 1998-05-13
49 PRIOR APPLICATION NUMBER: 60/085579
50 PRIOR FILING DATE: 1998-05-15
51 PRIOR APPLICATION NUMBER: 60/086392
52 PRIOR FILING DATE: 1998-05-22
53 PRIOR APPLICATION NUMBER: 60/089552
54 PRIOR FILING DATE: 1998-06-17
55 PRIOR APPLICATION NUMBER: 60/089538
56 PRIOR FILING DATE: 1998-06-17
57 PRIOR APPLICATION NUMBER: 60/089905
58 PRIOR FILING DATE: 1998-06-18
59 PRIOR APPLICATION NUMBER: 60/090472
60 PRIOR FILING DATE: 1998-06-24
61 PRIOR APPLICATION NUMBER: 60/090557

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PRIOR FILING DATE: 1998-06-24
 PRIOR APPLICATION NUMBER: 60/090691
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/090695
 PRIOR FILING DATE: 1998-06-25
 PRIOR APPLICATION NUMBER: 60/091982
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 PRIOR APPLICATION NUMBER: 60/095302
 PRIOR FILING DATE: 1998-08-04
 PRIOR APPLICATION NUMBER: 60/095318
 PRIOR FILING DATE: 1998-08-04
 PRIOR APPLICATION NUMBER: 60/095916
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 PRIOR APPLICATION NUMBER: 60/096146
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 PRIOR APPLICATION NUMBER: 60/097986
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 PRIOR FILING DATE: 1998-11-17
 PRIOR APPLICATION NUMBER: 60/108849
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 PRIOR APPLICATION NUMBER: 60/112422
 PRIOR FILING DATE: 1998-12-15

PRIOR APPLICATION NUMBER: 60/113296
 PRIOR FILING DATE: 1998-12-22
 PRIOR APPLICATION NUMBER: 60/113605
 PRIOR FILING DATE: 1998-12-23
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 PRIOR APPLICATION NUMBER: 60/115565
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/115733
 PRIOR FILING DATE: 1999-01-12
 PRIOR APPLICATION NUMBER: 60/119549
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 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: 60/125775
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 PRIOR APPLICATION NUMBER: 60/126773
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 PRIOR APPLICATION NUMBER: 60/166361
 PRIOR FILING DATE: 1999-11-16
 PRIOR APPLICATION NUMBER: 60/169445
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: 60/169495
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;
 Best Local Similarity 100.0%; Pred. No. 4,66-104;
 Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKNTLCTWSPGKETSYYQYVVKRTYAFGEKHNDCTNNTSSISENRA 60
 DB 52 ALPAKPNISCVYYRRKNTLCTWSPGKETSYYQYVVKRTYAFGEKHNDCTNNTSSISENRA 111

QY	6	SCSEFPLRITIPNNYITVEAENGSDVITSHNTYTRLENIATKEPPIFRKVPVLGIKRM	120
Db	112	SCSEFPLRITIPNNYITVEAENGSDVITSHNTYTRLENIATKEPPIFRKVPVLGIKRM	171
QY	121	IQIEMIKPELAPVSSDLKTYTLRFRYTVNSTSMNEVFAFKRKDKQNTYNLTGLQPFTEYVI	180
Db	172	IQIEMIKPELAPVSSDLKTYTLRFRYTVNSTSMNEVFAFKRKDKQNTYNLTGLQPFTEYVI	231
QY	181	ALRCVAKESKFWSDMSQEMKGMTEEPAP	208
Db	232	ALRCVAKESKFWSDMSQEMKGMTEEPAP	259
RESULT 4			
US-10-230-163-92			
Sequence 92, Application US/10230163			
Publication No. US2003003635A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Desnoyers, Luc			
APPLICANT: Gerritsen, Mary			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Grimaldi, J. Christopher			
APPLICANT: Gurney, Austin L.			
APPLICANT: Smith, Victoria			
APPLICANT: Stephan, Jean-Philippe F.			
APPLICANT: Matanabe, Colin L.			
APPLICANT: Wood, William I.			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
FILE REFERENCE: P3530PIC96			
CURRENT APPLICATION NUMBER: US/10/230,163			
CURRENT FILING DATE: 2002-08-28			
PRIOR APPLICATION NUMBER: 10/119,480			
PRIOR FILING DATE: 2002-04-09			
PRIOR APPLICATION NUMBER: 60/059113			
PRIOR FILING DATE: 1997-09-17			
PRIOR APPLICATION NUMBER: 60/062287			
PRIOR FILING DATE: 1997-10-17			
PRIOR APPLICATION NUMBER: 60/063549			
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PRIOR APPLICATION NUMBER: 60/064103			
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PRIOR APPLICATION NUMBER: 60/069873			
PRIOR FILING DATE: 1997-12-17			
PRIOR APPLICATION NUMBER: 60/078910			
PRIOR FILING DATE: 1998-03-20			
PRIOR APPLICATION NUMBER: 60/079294			
PRIOR FILING DATE: 1998-03-25			
PRIOR APPLICATION NUMBER: 60/079656			
PRIOR FILING DATE: 1998-03-26			
PRIOR APPLICATION NUMBER: 60/079728			
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PRIOR FILING DATE: 1998-06-17			

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PRIOR FILING DATE:	1998-06-18
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PRIOR FILING DATE:	1998-09-24
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PRIOR FILING DATE:	1998-10-29
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PRIOR APPLICATION NUMBER: 60/112442
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PRIOR APPLICATION NUMBER: 60/166361
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PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835
Query Match 100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4,6e-104;

Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALPAKPNISCVYYKRLCTWSPKETSYYQYTVKRYAFGEKHDNCTNSENRA 60
DB 52 ALPAKPNISCVYYKRLCTWSPKETSYYQYTVKRYAFGEKHDNCTNSENRA 111
QY 61 SCSPFLPRITIPDNTTIEVEANGDVIKSHMTYWRLENIATPEPKIFRVXVIGIKEM 120
DB 112 SCSPFLPRITIPDNTTIEVEANGDVIKSHMTYWRLENIATPEPKIFRVXVIGIKEM 171
QY 121 IOIEWTKPELAVSSDLKTLTFRYVNSTSWMEVNFAPKRRKRNQYNTLTGQPFTEYVI 180
DB 172 IOIEWTKPELAVSSDLKTLTFRYVNSTSWMEVNFAPKRRKRNQYNTLTGQPFTEYVI 231
QY 181 ALRCAYKESKFMWSOEGMGTEEBAP 208
DB 232 ALRCAYKESKFMWSOEGMGTEEBAP 259
RESULT 5
US-10-230-338-92
; Sequence 92, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Collin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-92
Query Match 100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4,6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALPAKPNISCVYYKRLCTWSPKETSYYQYTVKRYAFGEKHDNCTNSENRA 60

Db	Seq	Length
Db	52 ALPAKENISCVYYIKNMLCTGMSQKEISYQYIVKVTYAFGEKHDCITNSSTSENRA	111
Qy	61 SCSEFLPRITIPDNTYIEVEANGDGVIKSHMTYRLNIAKTEEPKIFRYKPLGIKRM	120
Db	112 SCSEFLPRITIPDNTYIEVEANGDGVIKSHMTYRLNIAKTEEPKIFRYKPLGIKRM	171
Qy	121 IQIEWIKPEIAPVSSDLKTYLRFRTYNSSTSMWVFAKRRDKQOTYNLTGLQFTFEVI	180
Db	172 IQIEWIKPEIAPVSSDLKTYLRFRTYNSSTSMWVFAKRRDKQOTYNLTGLQFTFEVI	231
Qy	181 ALRCAYKESKFWSDMSQEKMGTEEEAP	208
Db	232 ALRCAYKESKFWSDMSQEKMGTEEEAP	259

RESULT 6
US-10-218-631-92

Sequence 92, Application US/10218631
Publication No. US20030045687A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
FILE REFERENCE: P930P1C14
CURRENT APPLICATION NUMBER: US/10/218,631
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246

ORGANISM: Homo Sapien
US-10-218-631-92

Query Match	100.0%;	Score 1121;	DB 15;	Length 582;
Best Local Similarity	100.0%;	Pred. No. 4.6e-104;		
Matches 208; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0

Qy **1** ALPAKPENISCVYYRKNLTCTWSPGKETSTYQYTVKRTYAEGKHNDCTNMSSTSEKRA 60
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db **52** ALPAKPENISCVYYRKNLTCTWSPGKETSTYQYTVKRTYAEGKHNDCTNMSSTSEKRA 111
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy	6	SCSEFLPRTTIDPNTTIEVEANGGVKSHMTYWRLENIKTEBPPIPRKXPLVGIKRM	120
Db	112	SCSEFLPRTTIDPNTTIEVEANGGVKSHMTYWRLENIKTEBPPIPRKXPLVGIKRM	171
Qy	121	IQEWIKPELAPVSDLKTYLFRFVNSTSMWEVNFAPNRDKQNYNLGLQPFTEYVI	180
Db	172	IQEWIKPELAPVSDLKTYLFRFVNSTSMWEVNFAPNRDKQNYNLGLQPFTEYVI	231
Qy	181	ALRCAYKESKFMDSQEKMGTEEBAP	208
Db	232	ALRCAYKESKFMDSQEKMGTEEBAP	259

RESULT 7
US-10-230-414-92

Sequence 92, Application US/1020414
Publication No. US20030050448A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P9530PIC98
CURRENT APPLICATION NUMBER: US/10/230,414
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246

ORGANISM: Homo Sapien
US-10-230-414-92

Query Match	100.0%	Score 1121;	DB 15;	Length 582;
Best Local Similarity	100.0%	Pred. No. 4.6e-104;		
Matches 208; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

```
OY      I ALPAKPENISCVYYRRKNLTCTWSGKETSYQTYWKRFAFGEKDNCNTNSSTSENRA   60
        |||               |||||              |||||             |||||
DB      52 ALPAKPENISCVYYRKNLTC TWSPGKEYSYTQTYWKRTAFGEKXDCNCTNSSTSENRA 111
```

QY 61 SCSEFLPRITIPDNVTIEVEAENGVCISKHMTYRLLENIAKTEPKIFRVPVGLIKRM 120
DB 112 SCSEFLPRITIPDNVTIEVEAENGVCISKHMTYRLLENIAKTEPKIFRVPVGLIKRM 171

QY	121	IQIEMIKPELAVSSDLKTYTLRFRITVNSGSMSEVNFAKORKKDNQYTNLTGLQPFREYVI	180
Db	172	IQIEMIKPELAVSSDLKTYTLRFRITVNSGSMSEVNFAKORKKDNQYTNLTGLQPFREYVI	231
QY	181	ALRCAYKESKPFWSDMGSOEKGMTTEAP	208
Db	232	ALRCAYKESKPFWSDMGSOEKGMTTEAP	259

RESULT 8
INC-10-21

```

US-10-216-159A-92
; Sequence 92, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Wacanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P16
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: prt
; ORGANISM: Homo Sapien
US-10-216-159A-92

```

	Query Match	100.0%	Score 1121;	DB 15;	Length 582;
	Best Local Similarity	100.0%;	Pred. No. 4,6e-104;		
	Matches	208;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
QY	1	ALPAKENTSCVYYRKNLCTWS	PKGKENS	SYTYVKRYTA	FGEKDNCNTTSSSENRA 60
Db	52	ALPAPKENISCVYYRNKLCTWS	PKGKETS	SYTYVKRYTA	FGEKDNCNTTSSSENRA 111
QY	61	SCSFFLPRTIPDNYTIYEVAENGDDVIYSHTMYRLLENIAKTPEPKIFPVKVLGIKRM 120			
Db	112	SCSFELPRITIPDNYTIYEVAENGDDVISHTMYRLLENIAKTPEPKIFPVKVLGIKRM 171			
QY	121	IQIEMTKPELAPSDDKTYTLRRRTNSTNSWMEVFNAKORKDNQNYNLGLGPTEHYVI 180			

Db 172 IQEWMKPELAPPSLSLKTTLFRFVNSTSMENVPANRDKQTNLTSLQGFTEYVI 231

Qy 181 ALRCAYKESKFWSDMSQEGKMGTEBEAP 208

Db 232 ALRCAYKESKFWSDMSQEGKMGTEBEAP 259

RESULT 9

```

US-10-218-849-92
; Sequence 92, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Geriltsen, Marc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Matanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-92

```

Query Match	100.0%	Score 1121	DB 15	Length 582
Best Local Similarity	100.0%	Pred. No. 4,6e-104		
Matches	208	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	1	ALPAKPNISCVYYRRKRLICTWSPGKETSTGYTQTVKRTYAFGEKHDCNTNNSSTSENRA	60	
Db	52	ALPAKPNISCVYYRRKRLICTWSPGKETSTGYTQTVKRTYAFGEKHDCNTNNSSTSENRA	111	
QY	61	SCSFLLPRTTIDPDYTTIEVEAENDGVKSHMTYWRLENIKATBEPKIFRYVYVGIKRM	120	
Db	112	SCSFLLPRTTIDPDYTTIEVEAENDGVKSHMTYWRLENIKATBEPKIFRYVYVGIKRM	171	
QY	121	IQIEMIKRELPAVSSDLKYTLRFTVNSTSWMEYVAFARRDKQNTYMLTGLQPTFEYVI	180	
Db	172	IQIEMIKRELPAVSSDLKYTLRFTVNSTSWMEYVAFARRDKQNTYMLTGLQPTFEYVI	231	
QY	181	ALRCAYVESKFWSDMSQEKMGMTTEEAR	208	
Db	232	ALRCAYVESKFWSDMSQEKMGMTTEEAR	259	

RESULT 10

US-10-227-873-92
 : Sequence 92, Application US/1022787392
 : Publication No. US20030073816A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Baker, Kevin P.
 :
 : APPLICANT: Desnoyers, Luc
 :
 : APPLICANT: Gerritsen, Mary
 :
 : APPLICANT: Goddard, Audrey
 :
 : APPLICANT: Godowski, Paul J.
 :
 : APPLICANT: Grimaldi, J. Christophe
 :
 : APPLICANT: Gurney, Austin L.
 :
 : APPLICANT: Smith, Victoria
 :
 : APPLICANT: Stephan, Jean-Philippe
 :
 : APPLICANT: Matanabe, Colin B.
 :
 : APPLICANT: Wood, William I.

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P350P1C72
;; CURRENT APPLICATION NUMBER: US/10/227, 873
;; PRIOR APPLICATION NUMBER: 2002-08-26
;; PRIOR FILING DATE: 2002-04-09
;; PRIOR APPLICATION NUMBER: 60/059113
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/062287
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063549
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/064103
;; PRIOR FILING DATE: 1997-10-31
;; PRIOR APPLICATION NUMBER: 60/069873
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081955
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082804
;; PRIOR FILING DATE: 1998-04-22
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086392
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089905
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090691
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/095302
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095316
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095916
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/096146
;; PRIOR FILING DATE: 1998-08-11
;; PRIOR APPLICATION NUMBER: 60/096791
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 60/097986
;; PRIOR FILING DATE: 1998-08-26
;; PRIOR APPLICATION NUMBER: 60/098544
;; PRIOR FILING DATE: 1998-08-31
;; PRIOR APPLICATION NUMBER: 60/099596
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099598
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099811
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099812
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099816
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100038
;; PRIOR FILING DATE: 1998-09-11
;; PRIOR APPLICATION NUMBER: 60/100385
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100627
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: 60/100848
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/100919
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101477
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101786
;; PRIOR FILING DATE: 1998-09-25
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101922
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/106178
;; PRIOR FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/106248
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 60/106464
;; PRIOR FILING DATE: 1998-10-30
;; PRIOR APPLICATION NUMBER: 60/106905
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/108787
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108801
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112422
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/113605
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119549
;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/125259
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232

PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/111270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/111291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/111445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/114287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4,6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRNLTCTWSPKKETSYYQYVYKRTAFGEKDNCTNSTSENRA 60
DB 52 ALPAKPNISCVYYRRNLTCTWSPKKETSYYQYVYKRTAFGEKDNCTNSTSENRA 111
QY 61 SCSEFLPRITIPNYTTEVEAENDGVYKSHMTYWRLENTAKTEPPKIFVKGVLGIKRM 120
DB 112 SCSEFLPRITIPNYTTEVEAENDGVYKSHMTYWRLENTAKTEPPKIFVKGVLGIKRM 171
QY 121 IQIEWIKPELAPVSDIKYTLRFRYVNSTSMWEVNPANRKNKQNYNLGLQPFTEYVI 180
DB 172 IQIEWIKPELAPVSDIKYTLRFRYVNSTSMWEVNPANRKNKQNYNLGLQPFTEYVI 231
QY 181 ALRCAYESKFSWSDMGSEKMGTEEARP 208
DB 232 ALRCAYESKFSWSDMGSEKMGTEEARP 259

RESULT 11
US-10-227-883-92
Sequence 92, Application US/10227883
Publication No. US20030073817A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Geritlsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PIC78
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089905
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
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; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.6e-104; Indels 0; Gaps 0;
Matches 208; Conservative 0; Mismatches 0;

QY 1 ALPAXENISCVYYRKNLTCTWSPGKETSYYQYVYKRYAFGEKHDNCTTNSSTSENRA 60
DB 52 ALPAXENISCVYYRKNLTCTWSPGKETSYYQYVYKRYAFGEKHDNCTTNSSTSENRA 111
QY 61 SCGFLLPRTITPDNYTIEVEAENGVDVIRKSHMTYRLENIATPEPKIRVXPVIGIKM 120
DB 112 SCGFLLPRTITPDNYTIEVEAENGVDVIRKSHMTYRLENIATPEPKIRVXPVIGIKM 171
QY 121 IOEWIKPELAPSSSLKTLTFRRTYNSTSMWEVNAFKRKNQYTNLTGLOPFTYEVY 180
DB 172 IOEWIKPELAPSSSLKTLTFRRTYNSTSMWEVNAFKRKNQYTNLTGLOPFTYEVY 231
QY 181 ALRCAYKESKFWSDMSQEKMGTEBEAP 208
DB 232 ALRCAYKESKFWSDMSQEKMGTEBEAP 259

RESULT 12
US-10-219-076-92
; Sequence 92, Application US/10219076
; Publication No. US20030078379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C62
; CURRENT APPLICATION NUMBER: US/10/219,076
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; PRIOR FILING DATE: 2002-04-09
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; PRIOR FILING DATE: 1997-10-31
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; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/079294
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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-076-92

Query Match      100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4,6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRRKNTCTWSPKETSYYQYVRYVAFGEKDNCTNSISENRA 60
DB 52 ALPAKPNISCVYYRRKNTCTWSPKETSYYQYVRYVAFGEKDNCTNSISENRA 111
QY 61 SCSEPLPRTITPNNTTEVAENGDDGVTKSHMTYWRLENTAKTEPPKIFVKVLGIKRM 120
DB 112 SCSEPLPRTITPNNTTEVAENGDDGVTKSHMTYWRLENTAKTEPPKIFVKVLGIKRM 171
QY 121 IQEMIKELAPVSSDKYTLRFRVNSTSMMEVNFPAKKNQKQNTNLGLOPTEYVY 180
DB 172 IQEMIKELAPVSSDKYTLRFRVNSTSMMEVNFPAKKNQKQNTNLGLOPTEYVY 231
QY 181 ALRCAVSKSFWSQKMGTEENAP 208
DB 232 ALRCAVSKSFWSQKMGTEENAP 259
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C82
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PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4,6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKRENTSCVYYKNTCTWSPKETSQYTYKRYARFGKHNDCTSSSENNA 60
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DB 52 ALPAKRENTSCVYYKNTCTWSPKETSQYTYKRYARFGKHNDCTSSSENNA 111
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QY 61 SCFFLPRTITPDNTTYIEVEAENGQVIXSHNTYWRLENIATTEPKIFRVAPVLGIKIM 120
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DB 112 SCFFLPRTITPDNTTYIEVEAENGQVIXSHNTYWRLENIATTEPKIFRVAPVLGIKIM 171
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QY 121 IQIEWIKPELAPVSSDLKTLRPRYNTSMEVNFAPKRRKDNQTYNLTGLOPTEYVI 180
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DB 172 IQIEWIKPELAPVSSDLKTLRFRYNTSMEVNFAPKRRKDNQTYNLTGLOPTEYVI 231
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QY 181 ALRCAYKESKFWSDWSQERMGTEEBAP 208
|||||
DB 232 ALRCAYKESKFWSDWSQERMGTEEBAP 259
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RESULT 14
US-10-219-003-92
; Sequence 92, Application US/10219003
; Publication No. US20030088063A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, V. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C12
CURRENT FILING DATE: 2002-08-12
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; PRIOR APPLICATION NUMBER: 60/123618
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; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRKNLCTWSPGKETSQYTVKRTYAFGEKHNDCTNNSSENRA 60
DB 52 ALPAKPNISCVYYRKNLCTWSPGKETSQYTVKRTYAFGEKHNDCTNNSSENRA 111
QY 61 SCSEFLPRITIPDNYTTEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 120
DB 112 SCSEFLPRITIPDNYTTEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 171
QY 121 IOIEMIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRNKDKQNTNLTGLQPFTEYVI 180
DB 172 IOIEMIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRNKDKQNTNLTGLQPFTEYVI 231
QY 181 ALRCAVSKSKFWSQKMGTEBEAP 208
DB 232 ALRCAVSKSKFWSQKMGTEBEAP 259
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RESULT 15
US-10-219-075-92
; Sequence 92. Application US/10219075
; Publication No. US20030088064A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurley, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C61
; CURRENT APPLICATION NUMBER: US/10/219,075
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 92
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-075-92

Query Match      100.0%; Score 1121; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.6e-104;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALPAKPNISCVYYRKNLCTWSPGKETSQYTVKRTYAFGEKHNDCTNNSSENRA 60
DB 52 ALPAKPNISCVYYRKNLCTWSPGKETSQYTVKRTYAFGEKHNDCTNNSSENRA 111
QY 61 SCSEFLPRITIPDNYTTEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 120
DB 112 SCSEFLPRITIPDNYTTEVEAENGDVYKSHMTYWRLENIATPEPKIFRVKPVLGIGKM 171
QY 121 IOIEMIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRNKDKQNTNLTGLQPFTEYVI 180
DB 172 IOIEMIKPELAPVSSDLKTYTLRFTVNSTSMWEVNFAPKRNKDKQNTNLTGLQPFTEYVI 231
QY 181 ALRCAVSKSKFWSQKMGTEBEAP 208
DB 232 ALRCAVSKSKFWSQKMGTEBEAP 259
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Search completed: August 18, 2003, 13:33:22
Job time : 28.5067 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: August 18, 2003, 13:23:02 ; Search time 29.1496 Seconds
(without alignments)
686.221 Million cell updates/sec

Title: US-09-892-949-2_COPY_20_227

Perfect score: 1121

Sequence: 1 ALPAKPNISCVYYRKNLT.....SKFSDWSQEKMGTEEARP 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	271.5	24.2	917	2 149699	glycoprotein 130 -
2	268.5	24.0	918	2 A36337	membrane glycoprot
3	260	22.3	918	2 A44257	interleukin-6 sign
4	191	17.0	292	2 177525	prolactin receptor
5	191	17.0	303	2 177524	prolactin receptor
6	191	17.0	608	2 153269	prolactin receptor
7	190.5	17.0	830	2 150455	prolactin receptor
8	183	16.3	581	2 145971	prolactin receptor
9	181	16.1	310	2 A29884	prolactin receptor
10	181	16.1	412	2 A41070	prolactin receptor
11	181	16.1	610	2 A34631	prolactin receptor
12	181	16.1	610	2 A36116	prolactin receptor
13	179.5	16.0	831	2 J01655	prolactin receptor
14	169	15.1	616	2 A30304	prolactin receptor
15	166	14.8	771	2 B38252	granulocyte colony
16	166	14.8	783	2 JH0329	granulocyte colony
17	166	14.8	863	2 C38252	granulocyte colony
18	153	13.6	288	2 B59405	prolactin receptor
19	153	13.6	376	2 A59405	prolactin receptor
20	153	13.6	622	2 A40144	prolactin receptor
21	152.5	13.6	1097	2 S17308	leukemia inhibitor
22	151	13.5	837	2 A34898	granulocyte colony
23	150.5	13.4	372	2 158141	ciliary neurotroph
24	150.5	13.4	1092	2 JX0312	differentiation-st
25	150	13.4	630	2 151086	prolactin receptor
26	143.5	12.8	372	1 UHHCN	ciliary neurotroph
27	142	12.7	422	2 137891	interleukin-11 rec
28	140.5	12.5	432	2 148343	interleukin-11 rec
29	138.5	12.4	348	2 JCT907	common cytokine re

30	127.5	11.4	362	2 S60614	growth promoting a
31	124	11.1	1825	2 C88400	protein H19M22.1 l
32	124	11.1	1825	2 T32828	hypothetical prote
33	122.5	10.9	426	2 JCT773	IL-13Ralpha 1 prot
34	121.5	10.8	468	1 A41242	interleukin-6 rece
35	121	10.8	878	1 A40091	interleukin-3 rece
36	120	10.7	26926	1 B38344	cardiac mus
37	117.5	10.5	638	2 B28176	somatotropin recep
38	117.5	10.5	1162	2 PC4184	leptin receptor, O
39	117	10.4	440	2 JI0144	interleukin-6 rece
40	117	10.4	460	2 JI0145	interleukin-6 rece
41	116	10.3	896	1 A35782	cytokine receptor
42	115	10.3	897	1 A39255	cytokine receptor
43	114	10.2	608	2 S32823	somatotropin recep
44	113.5	10.1	638	2 S12136	somatotropin recep
45	112.5	10.0	531	2 S20900	titin - mouse (fra

ALIGNMENTS

RESULT 1
149699
glycoprotein 130 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
C:Accession: 149699; 148370
R:Saito, M.; Yoshida, K.; Hibi, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148: 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: 148370; MUID:92291532; PMID:1602143
A:Accession: 149699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-References: GB:M83336, NID:9193591; PIDN:AAA37723.1; PID:9193592
A:Accession: 148370
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-References: EMBL:X62646; NID:9840816; PIDN:CAA44515.1; PID:9840817
C:Genetics:
A:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>
Query Match 24.2%; Score 271.5; DB 2; Length 917;
Best Local Similarity 31.4%; Pred. No. 2.3e-15;
Matches 66; Conservative 45; Mismatches 84; Indels 15; Gaps 9;
QY 3 PAKPNISCVYYRKNLTCTSPKGETSY-TOYTKRYTAAFEKDKDNCCTNSTENRAS 61
DB 126 PKKPTNLTCTVEAGNLCOMDPGRETYLETNYTKSFWA-TEKPPDQSKHGT-----S 179
QY 62 GSF-FLPRTIPDNTIEVEAENGGVAKSHMTYRLENIATETPKIFRYKPVVGIKRM 120
DB 180 CAVSTMPITYV--NLEWVEAENALGKVSSEINFDVDPKVPPTPYNLSTVNSELSI 237
QY 121 IOIEWIKELAVSSDLKYTLFRFTVNSTSWMEVPAKRRDKQNTYMLTGQPTFEYVI 180
DB 238 LKLSWVSSGLGGL-LDLKSDIQRTKDASTWIGVPL-EDTWSPTRTSFTVQDKPTEYVF 295
QY 181 ALRCAYKES--KFNDSWQEKMGTEEARP 208
DB 296 RIR-SIKOSGKGWSDWSSEASGTYEDRP 324
RESULT 2
A36337
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000

C:Accession: J36337
R:Hihi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130
A:Reference number: A36337, MUID:91084844, PMID:2261637
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HTB>
A:Cross-references: GB:M57230, NID:g186353, PIDD:AA59155.1, PID:g186354
C:Genetics:
A:Gene: GDB:IL6ST, GP130
A:Cross-references: GDB:126725, OMIM:600694
A:Map position: Sq11-Sq11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:13-316/Domain: cytokine receptor homology <CRS>

Query Match	24.0%;	Score 268.5;	DB 2;	Length 918;
Best Local Similarity	30.3%;	Pred. No. 4.1e-15;		
Matches	66;	Conservative	47;	Mismatches 76;
			Indels	29;
			Gaps	11;

[illegible]

Dy 53 SSTSENKASCSFELPRITIPDNVYTEVEAENGDGYS-KS-HNTYWRLENIATKEPPPKFRV 111
|| : ||| : | : : ||
Db 186 YST-----VFV-----NIEWVAEALAGKTSDHINFDPYKV-KENPNHLSTV 230

Dy 112 KPVLGKIKMIQIEMIKPELAPVSSDLKYTLRFRITNSTSMWEVNFAKORUKONQTNLGTG 171
 : ::: | : | || ::::| ::::| : : :
 Db 231 INSEELSLKLKTWTNPSTKSIVI-LKYNQYRTKDASTNSQIP-PEDTASTRSSFTVQD 288

```
QY      172 LQFTTEYIALRCAYKESK-FWSDMSQCKMGMTTEBPAP 208  
       |:||||| :|| :: ||||| :| :| :|  
Db      289 LKFTTEYVRIKMKEDGKGWSDMSEASGITTEHP 326
```

RESULT 3

interleukin-6 signal transducing molecule gp130 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C/Accession: A44257
C/Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.

A;Title: Molecular cloning and characterization of the rat liver IL-6 signal transducing
A;Reference number: A44257; MUID:93052397; PMID:1427893
A;Accession: A44257

A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <MAN>

A: Experimental source: liver
A: Note: sequence extracted from NCBI backbone (NCBIP:118488)
C: Superfamily: cytokine receptor homology

F;134-315/Domain: cytokine receptor homology <CRS>

Query Match	22.3%	Score 250;	DB 2;	Length 918;
Best Local Similarity	31.4%;	Pred. No. 1.6e-13;		
Matches 66;	Conservative 42;	Mismatches 88;	Indels 14;	Gaps 9

QY 3 PAKENISCIYYRRKALITCTWSPKETSY -TQTVKRIFAEGEKHDCNTTNSSTENRAS 61
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 126 PDIPNLSCLVNEGKNMLCQLDPGRETYLETNTTLKSNA -TEKFPDCCRKHGTS ----S 18

Dy 62 CSF-FLPRITIPDNVTIEVEAENGDCVICKHMTWLELNIAKTEPPKIFRYKPVLTGIKRM 120
| : | : | : |||| : : : | : ||
Db 181 CMNGYTPRIYFV--NIEWWEAEALNAGNVSEPIINPVDKKPSPPHLNSTNSEELSTI 238

Db 233 LKAWNSGLDILR-LKSDIOYRKDKASTIQLVPL-EDTVSPRTSTFYQDLKPFIEYVF 236

Qy 181 ALRCAYKES--KFNDSMSQEKMGMTTEAP 208
:|::||:|||||:| | | | |
Db 297 RLR-STIKENGKGYMSDMSEASGTTYEDRP 325

RESULT 4

prolactin receptor precursor - mouse
C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision
C;Accession: I77525

R.; Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989

A1:Title: Expression of multiple forms of the prolactin receptor in mouse liver
 A1:Reference number: 1576699; MUID:89261824; PMID:2725531
 A1:Accession: 177535

A/Accession: 171525
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A:Cross-references: GB:M22959; NID:q200481; PIDN:AAA39977.1; PID:q2004822

C/Superfamily: cytokine receptor homology
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match	Score	DB 2	Length
17.0%	191	2	292

Best Local Similarity 27.8%; Pred. NO. 4.7e-09;
Matches 57; Conservative 38; Mismatches 92; Indels 18; Gaps 10;

db 23 PKKEIKHKRSPDKETFTCMWNPGSGLPTNYSL--TYSKEGEKNTYECPPDYKTSGPN- 79

Db 80 -SCFESKQYTSIMKIYIIITVNATNEMGSSITSDPLVDVTIIVEPEPPRNLTLEVKQLDKD 138

Qy 118 KRMIGIEWLKPELAPVSS---DLKTLRPFTVNISWMEVAFKKRKDKINQYINLTGQP 174
| : :: | : : : : : : : : : :
Db 139 KTVLMVKWLPPTITDVKTGMFTMEYEIRLKSEADWE-EIHFTGHQTQ---FKVPDLYP 193

QY 175 FTEVIALRCAYKESKFMSDMSQEK 199
 ::: | : |||
Db 194 GQKYLVTQRCK-PDHGYWSRWGQEK 217

RESULT 5

prolactin receptor precursor - mouse
C:Species: Mus musculus (house mouse)

CiDate: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000
CiAccession: I77524

R.; Davis, J.A.; Linzer, D.I.H.
Mol. Endocrinol. 3, 674-680, 1989

Title: Expression of multiple forms of the prolactin receptor in mouse liver
Accession number: 157639; MUID:89261824; PMID:2725531

A:Accession: I/7524
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Cross-references: GB:M22958; NID:q200479; PIDN:AAA3976.1; PID:q200480

C:Superfamily: cytokine receptor homology
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 17.0%; Score 191; DB 2; Length 303;

Best Local Similarity 27.8%; Pred. No. 4.9e-09;
Matches 57; Conservative 38; Mismatches 92; Indels 18; Gaps 10.

QY 3 PARENISCVYYRRKNLTCTWSPGKETS-YQTLYKRTYA-FGEKID-NCTINSSSTEINR 59
| | | : | | : | | : | | : |
DB 23 PKGREIHKKRS.PDKETFTCMWNPSGDGLPTNYSL--TYSKEGEKNTYECPDYKTSGBN- 79

0y 60 ASCSFFLPRTIPDNYTIEVEAENDGVIKSHMTYRWLENIAKTEPPK--IFRVKPYLGI 117

Db 80 -SCFSSQKYSITWIKYIITVANAENMGSSDPLVDVYIYVEPEPRNLTLEVKQDK 138

Qy 118 KRMIDIEWIKPELAPVSS--DLKYLTRRTYNSTSWMEVNFARKRDKQYTNLTGLQP 174

Db 139 KTYLWVWKMLPPTILTYKGTGFTMEYERLRKSEADEW-EIHFHQOTO----FKVDPLY 193

Qy 175 FTEYIALRCVAVSKESKFMDSWQOEK 199

Db 194 GQKIVQTRCK-PDHGIMSRMGQEK 217

RESULT 6

Prolactin receptor, long form - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 28-Jul-2000
 C.Accession: I53269; U06711; S34356
 R.Clark, D.L.; Linzer, D.I.H.
 Endocrinology 133, 224-232, 1993
 A.Title: Changes in prolactin receptor expression during pregnancy in the mouse ovary.
 A.Reference number: I53269; PMID:93307149; PMID:8319571
 A.Accession: I53269
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-608 <RES>
 A.Cross-references: GB:LI4811; NID:G293769; PIDN:AAA02686.1; PID:G293770
 R.Moore, R.C.; Oka, T.
 Gene 134, 263-265, 1993
 A.Title: Cloning and sequencing of the cDNA encoding the murine mammary gland long-form
 A.Reference number: U06711; MUID:94085788; PMID:8262385
 A.Accession: U06711
 A.Molecule type: mRNA
 A.Residues: 1-608 <MOO>
 A.Cross-references: GB:LI3593; NID:G347398; PIDN:AAC37641.1; PID:G347842
 R.Edery, M.; Pezet, A.; Nandi, S.; Kelly, P.A.
 submitted to the EMBL Data Library, June 1993
 A.Description: Isolation and nucleotide sequence of a mouse cDNA prolactin receptor.
 A.Reference number: S34356
 A.Accession: S34356
 A.Molecule type: mRNA
 A.Residues: 1-557, 'F', 559-608 <EDE>
 A.Cross-references: EMBL:X73372; NID:G312696; PIDN:CAA51789.1; PID:G312697
 C.Comment: Prolactin receptor have long form and short form which are resulted from altform
 C.Comment: This long form receptor is capable of transducing a signal to milk protein gene
 C.Superfamily: cytokine receptor homology
 C.Keywords: receptor; transmembrane protein
 F:31-216/Domain: cytosolic receptor homology <CRS>
 F:230-253/Domain: transmembrane #status predicted <TM>

	17.0%;	Score 191;	DB 2;	Length 608;
Query Match Similarity	27.8%;	Pred. No. 1,2e-08;		
Best Local	57;	Conservative 38;	Mismatches 92;	Indels 18;
Matches			Gaps	10;
QY	3	PAKPENISCVYYRRKRLTCTWSPEKETS-YTOYIVKRTYA-FGEKHD-NCTNSTSISNR	59	
DB	23	PGKPEIHKCRSPDKCTFTCTWNPSCSDGLPTVSL--TYSKEGEKNYTECPDYKTSGBN-	79	
QY	60	ASCSFELRLITPDYITTEVEENDDGYIKSMITWRLKLENIAKTEPPK-IFRYVPVAGI	117	
DB	80	-SCFSKQYTSIMKIYIIITVATNMGSTSDPLVDVATYVPEPPNNLTLEVQOLDK	138	
QY	118	KRMIDIEWIKPELAVSS--DLKTLRLFRITVNSTSMSEVNFAPKRRKDKNQTYNLTGLOP	174	
DB	139	KTYLWVKWKLPRITVDYKTGMFTMEYIRLKKSEADEW-EIHHTGQGTQ----FKVFDLYP	193	
QY	175	FTEYVIALRCAYKESKPFWSMGQEK	199	
DB	194	GQKYIVQTRCK-PDHGYVSRMGQEK	217	

RESULT 7

150455

prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C:Accession: 150455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor
A:Reference number: 150455; MUID:94283267; PMID:7516866
A:Accession: 150455
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CH2>
A:Cross-references: EMBL:U07694; NID:G466381; PIDN:AAA20646.1; PID:G466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match

[illegible]

RESULT 8

prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A>Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin
A:Reference number: I45971; MUID:93246019; PMID:1338725
A:Accession: I45971
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:I02549; NID:g163617; PIDN:AAAS1417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>

Query Match	16.3%	Score 183;	DB 2;	length 581;
Best Local Similarity	28.9%	Pred. NC. 5.4e-08;		
Matches 61;	Conservative 28;	Mismatches 90;	Indels 32;	Gaps 12

```

QY      3 PAKPENISCVYYRKNLTCTWSPGETSY--IQYTVKRTY-AFGAK--HDNCTNSNSTSE
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      28 PEKPKLVKCRSPKETFTCWMEPGADGGLPTNYTL--TYHKEGPTLIHE--CPDYKTGGR

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QY      59 RASGSFFLPRTITPDNYTTEVEAENGDDGVTKSHMTYWRLENIAKTEPPKIFRV----- 111
      ||| :| | | | | | | :| | | | | | | :| | | | | | | :
Db      85 --SCYFSKHTSINMYVTVNAINQMGISSDPLVHVHTYIIVEPPRANLTLELKHPE 142

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0y      112  -KPLVGIKMIQIEMIKPELAPVSSD---KYTLTFRFTVNSTSMWEVNFAPKRKDKNQTY 167
        |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      143  RKPLVLMIK-----WSPPTMTDVKSGWFIQYBIRAKPEKATDW--ETHFTL----KQTQL 191

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Db 404 KYIQIHCKPDHGSNSWSSE 425

Matches	64;	Conservative	22;	Mismatches	96;	Indels	54;	Gaps	10;
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Qy      3 PAKPENISCVYYRKNLT-----CTWSPGKETSJ-TQYVYKRTYAFGEKHNDCTNSST- 55
Db      123 PAIPHNLSCL-----MNLTSLSLIQWEPGPETHLPFSFTLKSPKSRG---NCOTQDSDI 174
Qy      56 -----SENBRASCSEFLPRITIPNDYITEVAENGDVYKSHMTYWRLENIAKTEPPKIFR 110
Db      175 LDCVPKDGQSHCCI PRKHLLIYQNMGIWQAENALGTSMSPOLCLDPMVDVKLEPPMLRT 234
Qy      111 VKPVLGIKRMIIQIEWIKPELAPVSS-----DLKYTLRFRTV-NSTSWME 153
Db      235 MDP-----SPEAAPPOAGCLQLCHEPWOGLHINQKCELRHKPQGEASWAL 281
Qy      154 VNFKNRKDNQYTNLTGLOPTEYIALRC-AVKESKFWSDSQEKMGTEEEAP 208
Db      282 VG---PLPLEALQYELCGLLPATAYTLQIRCIWRPLPGHWSWSPSLRLRTERAP 334

```

Search completed: August 18, 2003, 13:31:21
 Job time : 30.1496 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:27 ; Search time 15.81 Seconds
(without alignments)
618.695 Million cell updates/sec

Title: US-09-892-949-2_COPY_20_227

Perfect score: 1121
Sequence: 1 ALPAKPNISCVYYRKNLT.....SKFMSDWSQEKMGTEEAR 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt 41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271.5	24.2	917	IL6B_MOUSE	Q00560 mus musculu
2	268.5	24.0	918	IL6B_HUMAN	P40189 homo sapien
3	250	22.3	918	IL6B_RAT	P40190 rattus norv
4	191	17.0	608	PLR_MOUSE	Q08501 mus musculu
5	190.5	17.0	830	PLR_COLT	Q90374 columba liv
6	187	16.7	581	PLR_CEREL	Q28235 cervus elap
7	185	16.5	581	PLR_SHEEP	Q46561 ovis aries
8	184	16.4	862	IL2B_HUMAN	Q99665 homo sapien
9	183	16.3	581	PLR_BOVIN	Q28172 bos taurus
10	181	16.1	610	PLR_RAT	P05710 rattus norv
11	179.5	16.0	831	PLR_CHICK	Q04594 gallus gall
12	176.5	15.7	831	PLR_MELGA	Q91094 melagris g
13	174.5	15.6	874	IL2B_MOUSE	P97378 mus musculu
14	169	15.1	616	PLR_RABIT	P14787 oryctolagus
15	166	14.8	836	IL2B_MOUSE	Q99665 homo sapien
16	156.5	14.0	424	IL2B_MOUSE	Q09030 mus musculu
17	153	13.6	622	PLR_MOUSE	P16471 homo sapien
18	152.5	13.6	1097	IL2B_MOUSE	P42702 homo sapien
19	151	13.5	837	IL2B_MOUSE	P40223 mus musculu
20	150.5	13.4	372	IL2B_MOUSE	Q08406 rattus norv
21	150.5	13.4	1092	IL2B_MOUSE	P42703 mus musculu
22	150	13.4	630	IL2B_MOUSE	Q91513 oreochromis
23	143.5	12.8	372	IL2B_MOUSE	P26992 homo sapien
24	137	12.2	427	IL2B_MOUSE	P78552 homo sapien
25	127.5	11.4	362	IL2B_MOUSE	P51641 gallus gall
26	121.5	10.8	468	IL2B_MOUSE	P08887 homo sapien
27	121	10.8	380	IL2B_MOUSE	Q14627 homo sapien
28	121	10.8	878	IL2B_MOUSE	P26954 mus musculu
29	117.5	10.5	638	IL2B_MOUSE	P19941 oryctolagus
30	117.5	10.5	1162	IL2B_MOUSE	Q62959 rattus norv
31	117	10.4	460	IL2B_MOUSE	P22222 mus musculu
32	116	10.3	896	IL2B_MOUSE	P26955 mus musculu
33	115	10.3	897	IL2B_MOUSE	P32927 homo sapien

34	114	10.2	608	IL6B_MOUSE	Q02092 gallus gall
35	113.5	10.1	638	IL6B_MOUSE	P19756 sus scrofa
36	112.5	10.0	1162	IL6B_MOUSE	P48356 mus musculu
37	112	10.0	462	IL6B_MOUSE	P22273 rattus norv
38	112	10.0	537	IL6B_MOUSE	P26896 rattus norv
39	111.5	9.9	415	IL6B_MOUSE	P21183 mus musculu
40	110.5	9.9	1005	IL6B_MOUSE	P54757 rattus norv
41	109.5	9.8	507	IL6B_MOUSE	P14753 mus musculu
42	109	9.7	420	IL6B_MOUSE	Q01344 homo sapien
43	108.5	9.7	551	IL6B_MOUSE	P14784 homo sapien
44	107.5	9.6	638	IL6B_MOUSE	P10912 homo sapien
45	107	9.5	467	IL6B_MOUSE	O18796 sus scrofa

ALIGNMENTS

RESULT 1
ID IL6B_MOUSE STANDARD; PRT; 917 AA.
AC Q00560;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (Interleukin
DE 6 signal transducer) (Membrane glycoprotein 130) (GPI30).
GN IL6ST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1 Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=92291532; PubMed=1602143;
RA Saito M., Yoshida K., Hibl M., Taga T., Kishimoto T.;
RT "Molecular cloning of a murine IL-6 receptor-associated signal
RT transducer, GPI30, and its regulated expression in vivo.";
RT J. Immunol. 148:4066-4071(1992).
RL J. Immunol. 148:4066-4071(1992).
CC - FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, IL-1, IL-11 CAN UTILIZE GPI30 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT.
CC - SUBUNIT: Heterodimer of an alpha and a beta chain.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - TISSUE SPECIFICITY: FOUND IN TISSUES SUCH AS BRAIN, HEART, THYMUS,
CC SPLEEN, KIDNEY, LUNG AND LIVER. FOUND IN ALL THE CELL LINES TESTED
CC EXCEPT BAR-B03. EXPRESSION NOT RESTRICTED TO IL-6-RESPONSIVE
CC CELLS.
CC - DEVELOPMENTAL STAGE: IN EMBRYONIC STEM CELLS IT IS FOUND FROM DAY
CC 6 OF GASTRULATION. IT REACHES A PEAK ON DAY 8 AND GRADUALLY DECLINES
CC DURING THE REST OF EMBRYOGENESIS.
CC - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC - SIMILARITY: Contains 5 fibronectin type III domains.
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X62646; CAA44515.1; -
CC EMBL; M83336; AAA37723.1; -
CC PIR; I49699; I49699.
CC HSSP; P40189; 1B0V.
CC WGD; WGI:96560; 116EC.
CC GO; GO:0007165; P:signal transduction; IDA;
CC InterPro; IPR002996; CRIA.

DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003529; Hemtopocln_L_F2.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 5.
 DR PROSITE: PS01353; HEMATOPO REC_L_F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
 Repeat.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 917 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
 FT DOMAIN 23 617 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 618 639 POTENTIAL.
 FT DOMAIN 640 917 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 26 120 IG-LIKE C2-TYPE.
 FT DOMAIN 124 220 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 221 322 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 423 420 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 422 515 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 516 611 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 723 741 SER-RICH.
 FT DISULFID 28 54 By similarity.
 FT DISULFID 48 103 By similarity.
 FT DISULFID 134 144 By similarity.
 FT DISULFID 172 180 By similarity.
 FT DISULFID 456 464 By similarity.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 476 476 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 917 AA; 102452 MW; FCEED220BC466F4 CRC64;

Query Match 24.28; Score 271.5; DB 1; Length 917;
 Best Local Similarity 31.48; Pred. No. 1.6e-17;
 Matches 66; Conservative 45; Mismatches 84; Indels 15; Gaps 9;

QY 3 PAKPENISCVYYRKNLTCTWSPGKETS-TOYTKVTAFGKHNDCTTNSSTSENRAS 61
 DB 126 PDKPTNLCTVNEGKNMLCQMDPERETYLENTLTLSKEM-TEFPPCQSHGT-----S 179
 QY 62 CSF-FLEPRITPDYTTIEVAENGDAVGIKSMYTWRLNIAKTEPPKIFVKEVLGIKRM 120
 DB 180 CWSYMTYYV--NIEVWVAENALGKVSESEINPDVDKVKPTPPYNLSVTSEBSLSI 237
 QY 121 IQIEWIKPELAPVSSDLKTLRFTNSTGSMMEVNFANRKNQYNTLTGLOPFTERYT 180
 DB 238 LKDSWSSGLGGL-LDKSDIQYRTKASWTIQLPL-EDTMSPTSTFTVDLKPFEYVF 295
 QY 181 ALRCAYVES--KFWSDMSQKMGTEBEAP 208
 DB 296 RIR-SIKDSGKGWSDWSEBSAGTYEDRP 324

RESULT 2
 IL6B HUMAN
 ID IL6B HUMAN STANDARD; PRT; 918 AA.

AC P40189; Q9U041;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) [Interleukin
 6 signal transducer] (Membrane glycoprotein 130) (GP130) (Oncostatin M
 receptor) (CDW130) (CD130 antigen).
 GN IL6ST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Myeloma, and Placenta;
 RX MEDLINE=91084844; PubMed=2261637;
 RA Hibi M., Murakami M., Saito M., Hirano T., Taga T., Kishimoto T.;
 RT "Molecular cloning and expression of an IL-6 signal transducer,
 RT gp130.";
 RL Cell 63:1149-1157(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Synovium;
 RX MEDLINE=20341529; PubMed=10880057;
 RA Tanaka M., Kishimura M., Ozaki S., Osekada F., Hashimoto H., Okubo M.,
 RA Murakami M., Nakao K.;
 RT "Cloning of novel soluble gp130 and detection of its neutralizing
 RT autoantibodies in rheumatoid arthritis.";
 RL J. Clin. Invest. 106:137-144(2000).
 RN [3]
 RP PARTIAL SEQUENCE, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=2169388; PubMed=11098061;
 RA Moritz R.L., Hall N.E., Connolly L.M., Simpson R.J.;
 RT "Determination of the disulfide structure and N-glycosylation sites of
 RT the extracellular domain of the human signal transducer gp130.";
 RL J. Biol. Chem. 276:8244-8253(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 122-325.
 RX MEDLINE=98169383; PubMed=9501088;
 RA Bravo J., Staunton D., Heath J.K., Jones E.Y.;
 RT "Crystal structure of a cytokine-binding region of gp130.";
 RL EMBO J. 17:1665-1674(1998).
 CC -1- FUNCTION: Signal-transducing molecule. The receptor systems for
 CC IL-6, IL-6, OSM, CNTF, IL-11 AND CT-1 can utilize gp130 for
 CC initiating signal transduction. Binds to IL-6/IL-6-R (alpha chain)
 CC complex, resulting in the formation of high-affinity IL-6 binding
 CC sites, and transduces the signal. Does not bind IL-6. May have a
 CC role in embryonic development (By similarity).
 CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
 CC -1- Secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P40189-1; Sequence=Displayed;
 CC Name=2; Synonyms=Gp130-RAPs;
 CC IsoId=P40189-2; Sequence=VSP_001684;
 CC -1- TISSUE SPECIFICITY: Found in all the tissues and cell lines
 CC examined. Expression not restricted to IL-6 responsive cells.
 CC -1- DISBASE: Isoform 2 is an autoantigen found in rheumatoid arthritis
 CC (RA) but it is not specific to patients with RA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- DATABASE: NAME=PROM; NOTE=CD guide CD130 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd130.htm".
 CC -----
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 CC -----
 CC EMBL; M57230; AAA59155.1; -
 CC EMBL; AB015706; BAA78112.1; -
 CC PIR; A36337; A36337.
 CC DR PDB; 1B0U; 26-AUG-98.
 CC DR PDB; 1B08; 13-JAN-99.
 CC DR PDB; 1IIR; 28-MAR-01.
 CC DR Genew; HGNC:6021; IL6ST.
 CC MIM; 600694; -
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0004898; F:gp130; TAS.
 CC DR GO; GO:0004924; F:oncostatin-M receptor activity; TAS.
 CC DR GO; GO:0004872; F:receptor activity; TAS.

DR CO; GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003529; Hemtopoptn_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS01353; HEMATOPO REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
Repeat; 3d-structure; Alternative splicing.
FT SIGNAL 1 22
FT CHAIN 23 918 INTERLEUKIN-6 RECEPTOR BETA CHAIN.
FT DOMAIN 23 619 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 620 641 POTENTIAL.
FT DOMAIN 642 918 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 120 IG-LIKE C2-TYPE.
FT DOMAIN 124 222 FIBRONECTIN TYPE-III 1.
FT DOMAIN 223 324 FIBRONECTIN TYPE-III 2.
FT DOMAIN 325 423 FIBRONECTIN TYPE-III 3.
FT DOMAIN 424 517 FIBRONECTIN TYPE-III 4.
FT DOMAIN 518 613 FIBRONECTIN TYPE-III 5.
FT DOMAIN 725 755 SER-RICH.
FT DISULFID 28 54
FT DISULFID 48 103
FT DISULFID 134 144
FT DISULFID 172 182
FT DISULFID 458 466
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .)
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .)
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .)
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .)
FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .)
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .)
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .)
FT CARBOHYD 553 553 N-LINKED (GLCNAC. . .)
FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .)
FT VARSPLIC 325 329 RPSKA -> NIASP (1n isoform 2).
FT VARSPLIC 330 918 /Frid=VSP_001684.
Missing (in isoform 2).
/Frid=VSP_001685.
FT VARSPLIC 330 918
FT STRAND 130 137
FT TURN 138 139
FT STRAND 143 147
FT STRAND 157 164
FT TURN 165 166
FT STRAND 167 168
FT STRAND 172 173
FT TURN 179 180
FT STRAND 181 183
FT TURN 190 191
FT STRAND 194 202
FT TURN 203 204
FT STRAND 205 208
FT STRAND 212 214
FT HELIX 216 218
FT STRAND 220 221
FT STRAND 226 231
FT STRAND 240 245
FT HELIX 248 251
FT TURN 252 252
FT STRAND 264 265
FT STRAND 270 271
FT HELIX 274 277
FT STRAND 283 286
FT STRAND 293 303
FT TURN 304 305
FT STRAND 317 321
FT HELIX 325 331
SQ SEQUENCE 918 AA; 103522 MW; D813F3672DD10D53 CRC64;
Query Match 24.0%; Score 268.5; DB 1; Length 918;
Best Local Similarity 30.3%; Pred. No. 3e-17;

Matches 66; Conservative 47; Mismatches 76; Indels 29; Gaps 11;
QY 3 PAKENISCVYYRRKRLCTWSPGKSTY-TOYTK---RTYAFGS---KHP---NCTN 52
Db 126 PEKPNKLSCTVNEGKMKCEMGGRTHLETFTLKSEWATIKFADCKAKRTPTSCYVD 185
QY 53 SSTSENRRASCSPFLPRITIPDNYTIEVEANGDVYKS-HMTYMLNIAKTEPPKIFRV 111
Db 186 YST-----YFV-----NIEVWEAENALGKVTSDHINFDPPYKV-KENPNNLSV 230
QY 112 KAVLGIKRMIOLEWKPELAPVSDLKTLRRRTYNSISWMEVNAKAKKQNTYNTLG 171
Db 231 INSEBSSILKLTWNPSTKSYTI-LKYNIOYRTDASTWSQIP-PEDASTRSSPTV 288
QY 172 LQPTFEYVALACAVESK-FWSDMSQKMGWTESEAP 208
Db 289 LKPFTEYFRIRKMKEDGKGYSDWSEASGITYEDRP 326
RESULT 3
ID IL6B RAT STANDARD; PRT; 918 AA.
AC P40150;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (II-6R-beta) (Interleukin
6 signal transducer) (Membrane glycoprotein 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
transducing molecule, gp130.";
RL Genomics 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC -----
DR EMBL; M92340; -, NOT_ANNOTATED_CDS.
DR PIR; A44257; A44257.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003529; Hemtopoptn_L_F2.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS01353; HEMATOPO REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;

Query March	17.0%;	Score 191;	DB 1;	Length 608;
Best Local Similarity	27.8%;	Pred. No. 3.2e-10;		
Matches 57;	Conservative 38;	Mismatches 92;	Indels 18;	Gaps 10;

RESULT 5	
PRLR_COLL1	STANDARD;
ID_PRLR_COLL1	PRT; 830 AA

```

DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) .
GN PRLR.
OS Columba livia (Domestic pigeon) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_Taxid=8932;
[1]
RN SEQUENCE FROM N.A.
RP
RC TISSUE=CropSac;
RX MEDLINE=94283267; PubMed=7516866;
RA Chen X., Horsemann N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
RT receptor".
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
CC -----
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CC or send an email to license@isb-sb.ch) .

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Query Match	17.0%;	Score 190.5;	DB 1;	Length 830;
Best Local Similarity	27.9%;	Pred. No. 5.3e-10;		
Matches	57;	Conservative	27;	Mismatches 105;
			Indels	15;
			Gaps	6;

Qy 3 PAKENISICVYYAKNKLCTMSPEKENS-Y-QYVVKRYVARGKHNDNTTMSSTENAS 61
Db 232 PEKTTIKKNSPEKETFTCWKPKSPDGGHPYNTLLYSKGEERVYELCPDYKTAGN--S 289
Qy 62 CSFELPRITTPDNYTIEVEANGDGVIKSHMTYRLNIAKTEPP--KIFVKPPLGIKR 119
Db 290 CYFPKHTSEFTYINITYKATNELSGNSVSDLYDYVITYIGTDPVANTLEKTKVNRKP 349
Qy 120 MIQIEWIKPELIAPVS--DIKYTLLRPRTVNSTSMMEVNFANKRDKNQI-YNLGLQPF 175
Db 350 YLVLTWSPPLADVRSGWLTLDYELRLKPEEABEEMETIFVQ-----QTHYKMSLNP 403
Qy 176 TEYVIALRCANKESEFMSDMSQEK 199
Db 404 KRYIVQIHCKPDHHGHSWEWSLEK 427

	RESULT 6			
	PRLR_CEREL	STANDARD;	PRT;	581 AA.
ID	PRLR_CEREL			
AC	Q28235;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	Prolactin receptor precursor (PRL-R).			
GN	PRLR.			
OS	Cervus elaphus (Red deer).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Cervoidae;			
OC	Cervidae; Cervinae; Cervus.			
OX	NCBI_TaxID=9860;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=66030711; PubMed=7561644;			
RA	Clarke L.A., Beery M., Loudon A.S., Randall V.A., Poetel-Vinay M.C.			

RA Kelly P.A., Jabbour H.N.,
 RT "Expression of the prolactin receptor gene during the breeding and
 RT non-breeding seasons in red deer (*Cervus elaphus*): evidence for the
 RT expression of two forms in the testis.",
 RL J. Endocrinol. 146:313-321(1995).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X94953; CA64419.1; -.
 DR HSSP: P14787; IAN3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR003528; Hemtopoptn_L_F1.
 DR Pfam: PF00041; FN3; 2.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01352; HEMATOPO REC L_F1; 1.
 DR Receptor: Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 24
 FT CHAIN 25 581
 FT DOMAIN 25 234
 FT TRANSFEM 235 258
 FT DOMAIN 259 581
 FT DOMAIN 25 122
 FT DOMAIN 123 227
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 132 132
 FT CARBOHYD 233 233
 SO SEQUENCE 581 AA; 65159 MW; 975E47CB63CE28BC CRC64;
 Query Match 16.7%; Score 187; DB 1; Length 581;
 Best Local Similarity 29.9%; Pred. No. 7.1e-10;
 Matches 63; Conservative 27; Mismatches 89; Indels 32; Gaps 12;
 QY 3 PAKPENISCVYYKNTCTWSPGKENSY--TOYTVKRTY-AFGKK--HDNCTNNSSEN 58
 DB 28 PGRKXIKKCRSPGKETFTCMWEPESDGLPTNTL--TYKKEGTLIHE--CPDYKGTGPN 84
 QY 59 RASCSFPLPRITTPDNTYIEVANGDVVKSHTYWRLENIAKTEPPKIFRV----- 111
 DB 85 --TCYFSPKSKHTSIKIVITVNAIINQGVSSDPLYVDVYIYVEPPPAULTLELKHED 142
 QY 112 -KPLVGIKRMQIWIWELAPVSSD--LKYTRFTVNSTSMENFPAKRNKQNTY 167
 DB 143 RKPLMLWK-----WPPPTLTDVSGWFMQYERLKEPETAADW--EIHFAA---KOTOL 191
 QY 168 NLTGLOPTEYVIALRCVAVESKESQMSQSE 198
 DB 192 KIRSLYFGQKYLVOVRCK-PDHWGSMSPS 221
 RESULT 7
 PRLR SHEEP STANDARD; PRT; 581 AA.
 AC O46561; O46569; O46573; O46574; P79203; P79205;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (OPR).
 GN PRLR.
 OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_Taxid=9940;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Liver, and Mammary gland;
 RX MEDLINE=98001468; PubMed=9343303;
 RA Bignon C., Bihart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.,
 RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
 RT and genomic analysis reveal that the two forms arise by different
 RT alternative splicing mechanisms in ruminants and in rodents.",
 RL J. Mol. Endocrinol. 19:109-120(1997).
 RN [2]
 RP SEQUENCE OF 61-395 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
 RP SPECIFICITY.
 RC STRAIN=Scottish blackface; TISSUE=anterior pituitary;
 RX MEDLINE=99049302; PubMed=9832462;
 RA Tortorese D.J., Brooks J., Ingleton P.M., McNeilly A.S.,
 RT "Detection of prolactin receptor gene expression in the sheep
 RT pituitary gland and visualization of the specific translation of the
 RT signal in gonadotrophs.",
 RL Endocrinology 139:5215-5223(1998).
 RN [3]
 RP SEQUENCE OF 147-302 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Corpus luteum, and Fetal liver;
 RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.,
 RT "Two forms of the prolactin receptor messenger ribonucleic acid are
 RT present in ovine fetal liver and adult ovary.",
 RL Endocrine 3:291-295(1995).
 CC -1- FUNCTION: This is a receptor for the anterior pituitary hormone
 CC prolactin.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Long, L-OPR;
 CC IsoId=O46561-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short, S-OPR;
 CC IsoId=O46561-2; Sequence=VSP_001732, VSP_001733;
 CC Name=3; Synonyms=Soluble;
 CC IsoId=O46561-3; Sequence=VSP_001730, VSP_001731;
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined, liver,
 CC pituitary, adrenal gland, ovary and fetal liver.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 CC EMBL: AF041257; AAB96795.1; -.
 CC EMBL: AF041977; AAB96920.1; -.
 CC EMBL: AF041979; AAB97082.1; -.
 CC EMBL: AF042358; AAB97744.1; -.
 CC EMBL: AF042358; AAB97743.1; -.
 CC EMBL: AF041978; AAB96965.1; -.
 CC EMBL: Y10578; CAA71597.1; -.
 CC EMBL: Y10808; CAA71766.1; -.
 CC HSSP: P14787; IAN3.
 CC InterPro: IPR002996; CRIA.
 CC InterPro: IPR003961; FN.III.
 CC InterPro: IPR003528; Hemtopoptn_L_F1.
 CC Pfam: PF00041; FN3; 2.
 CC SMART: SM00060; FN3; 2.
 CC PROSITE: PS01352; HEMATOPO REC L_F1; 1.
 CC Receptor: Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing.
 FT SIGNAL 1 24
 FT SIGNAL 24 POTENTIAL.

FT CHAIN 25 581 PROLACTIN RECEPTOR.
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 24 66 GOSPEPPLIKRSGKFTGCMWRGADGCPNTYLY
 FT YLLLVTS (in isoform 3).
 FT VARSPPLIC 67 581 /FTId=VSP 001730.
 FT VARSPPLIC 286 296 Missing (in isoform 3).
 FT VARSPPLIC /FTId=VSP 001731.
 FT VARSPPLIC KGSSEBLRL -> ISQSRSLVSVF (in isoform 2).
 FT VARSPPLIC /FTId=VSP 001732.
 FT VARSPPLIC Missing (in isoform 2).
 FT CONFLICT 281 281 /FTId=VSP 001733.
 FT CONFLICT 387 387 I -> V (IN REF. 1; AAB97743/AAB97744).
 FT CONFLICT 581 AA; 65235 MW; EC534FDE538837A0 CRC64;
 SQ SEQUENCE

Query Match 16.5%; Score 185; DB 1; Length 581;
 Best Local Similarity 29.4%; Pred. No. 1.1e-09;
 Matches 65; Conservative 27; Mismatches 97; Indels 32; Gaps 12;

QY 3 PAKPENISCVYTYRKLTCTWSPGKETS-YQYTVKRTY-ARGEK-HDNCTNSTSEN 58
 DB 28 PEKPKLIKRSPEKFTGCMWRGADGCPNTYLY-TYKSEETLIH-CPDYKTCGN 84
 QY 59 RASCSFPLPRITIPDVTTEVEAENGDDGYKSHMTWRLNIAKTEPKIFRY----- 111
 DB 85 -SCYSSKTYTSWKWVITVSAINQMGISSDPLVYDVYLYVEPPVNLTELHGPED 142
 QY 112 -KPVLGIKRMIOLEWIKPELAPVS--DLKYLTRFTVNSTSWMEVNAKNDKQY 167
 DB 143 RKRYLMIK-----WSPPLTLDVKSQWPSIQYIIRLKEPATGW-ETHFA-----PLTLQL 191
 QY 168 NLTLGLOPTEYVIALNCVAVESKFSWDSQEKMGTEEAR 208
 DB 192 KIFNLPGQKYLVOIRCK-PDHGWSWSESPESFIQIPNDFP 231

RESULT 8
 ID 112S HUMAN STANDARD; PRT; 862 AA.
 AC Q99665;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2) (IL-12R-beta2).
 GN IL12RB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxId=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97098510; PubMed=8943050;
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y., Gately M.K., Gubler U.;
 RT "A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY.
 CC -1- SUBUNIT: DIMER/OLIGOMER, DISULFIDE-LINKED. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 3 fibronectin type III domains.
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 CC -----
 DR EMBL: U64198; AAB3675.1; -
 DR HSSP: P40189; 1BCU.
 DR Genew: HGNC:5972; IL12RB2.
 DR MIM: 601642; -
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0004907; F: interleukin receptor activity; TAS.
 DR GO: GO:0007166; P: cell surface receptor linked signal transdu. .; TAS.
 DR GO: GO:0008284; P: positive regulation of cell proliferation; TAS.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hemtopopln_L_F2.
 DR Pfam: PF00041; Fn3; 3.
 DR SMART: SM00060; FN3; 4.
 DR PROSITE: PS01353; HEMATOPO REC L_F2; 1.
 DR KMW: Receptor; Transmembrane; Glycoprotein; Signal; Repeat; Polymorphism.
 FT SIGNAL 1 21
 FT CHAIN 22 862
 FT DOMAIN 22 624
 FT TRANSMEM 625 641
 FT DOMAIN 642 862
 FT DOMAIN 224 306
 FT DOMAIN 421 508
 FT DOMAIN 519 607
 FT CARBOHYD 48 48
 FT CARBOHYD 129 129
 FT CARBOHYD 166 166
 FT CARBOHYD 195 195
 FT CARBOHYD 271 271
 FT CARBOHYD 347 347
 FT CARBOHYD 376 376
 FT CARBOHYD 480 480
 FT VARIANT 185 185
 FT VARIANT 420 420
 FT VARIANT 426 426
 FT VARIANT 465 465
 FT SEQUENCE 862 AA; 97134 MW; 67C0BD09468BD58 CRC64;
 SQ SEQUENCE

Query Match 16.4%; Score 184; DB 1; Length 862;
 Best Local Similarity 29.6%; Pred. No. 2.2e-09;
 Matches 64; Conservative 28; Mismatches 96; Indels 28; Gaps 10;

QY 3 PAKPENISCVYTYRKLTCTWSPGKETS-YQYTVKRTY-ARGEK-HDNCTNSTSEN 58
 DB 124 PEOPNLSCIOEGEAGTACTWGERGRDTHLYTEYLDS--GPK-NLTWQCKCK-I 176
 QY 61 SCSPF-----LPRITIPDVTTEVEAENGDDGYKSHMTWRLNIAKTEPKIFRYKPV 115
 DB 177 YCDYIDDFGINTLPBSPESNFTAKVAVNSLSSSSLPSTFTLDVRLPDPMDIKPKQ 236
 QY 116 GKRMIOLEWIKPELAPVSSDLKYLTRFTVNSTSWMEVNF-AKNDKQYVNLGLQ 173
 DB 237 ASVSRCTLYWRDEGLV-----LNLRLRYRPSRSRLMNVNVTAKGRHD-----LLDLK 285
 QY 174 PTEYVIALRCVAVESK-FWSDSQEKMGTEEAR 208
 DB 286 PTEYEFQISSLKHLHYKGSWDSSESRLAQTPPEEP 321

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RESULT 9
PRLR_BOVIN STANDARD; PRT; 581 AA.
ID Q28172; 018880; 046591;
AC Q28172; 018880; 046591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
PRLR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Endometrium;
RX MEDLINE=93246019; PubMed=1338725;
RA Scott P., Kessler M.A., Schuler L.A.;
RT "Molecular cloning of the bovine prolactin receptor and distribution
RT of prolactin and growth hormone receptor transcripts in fetal and
RT utero-placental tissues."
RL Mol. Cell. Endocrinol. 89:47-58(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY.
RC TISSUE=Endometrium;
RX MEDLINE=9375450; PubMed=9231767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
RT tissues."
RL Endocrinology 138:3187-3194(1997).
RN [3]
RP SEQUENCE OF 25-234 FROM N.A., AND SEQUENCE OF 25-33.
RC TISSUE=Mammary gland;
RX MEDLINE=95256770; PubMed=7738463;
RA Thelet A., Stalen N.R., Creely D.P., Krivi G.G., Gertler A.;
RT "Extracellular domain of prolactin receptor from bovine mammary gland:
RT expression in Escherichia coli, purification and characterization of
RT its interaction with lactogenic hormones."
RL J. Endocrinol. 144:393-403(1995).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=98001468; PubMed=9343303;
RA Blynon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Diane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
RT and genomic analysis reveal that the two forms arise by different
RT alternative splicing mechanisms in ruminants and in rodents."
RL J. Mol. Endocrinol. 19:109-120(1997).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q28172-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q28172-2; Sequence=VSP 001718, VSP 001719;
CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,
CC peripheral blood lymphocytes, endometrium, corpus luteum,
CC intestine, fetal thymus, fetal spleen, fetal liver and fetal
CC brain.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC -----

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DR EMBL; L02549; AAA51417.1; -.
DR EMBL; AF027403; AAB83999.1; -.
DR EMBL; AF042780; AAB97748.1; -.
DR EMBL; AF042780; AAB97747.1; ALT_SEQ.
DR PIR; I45971; I45971.
DR HSSP; P14787; IAN3.
DR InterPro; IPR002996; CRA.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemopoptn_L_F1.
DR Pfam; PR00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 237
FT TRANSMEM 238 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT VARSPLIC 266 296
FT FT
FT VARSPLIC 297 581
FT FT
FT COMPLECT 120 120
FT COMPLECT 128 128
FT COMPLECT 137 137
FT COMPLECT 141 141
FT COMPLECT 156 157
FT COMPLECT 186 186
SQ SEQUENCE 581 AA; 65153 MW; 7385CD0695EB139 CRC64;

Query Match 16.3%; Score 183; DB 1; Length 581;
Best Local Similarity 28.9%; Pred. No. 1,7e-09;
Matches 61; Conservative 28; Mismatches 90; Indels 32; Gaps 12;

QY 3 PAKPENISCVYYRKNLTCTWSPGKRTSY-TOYIVKRY-ARGEK--HDNCTNSTSEN 58
DB 28 PEKPKLVKRSPOKERTFTCMWEPGADGLPTVYTL--TYHKGERTLIHE-CPDYKTCGPN 84
QY 59 RASGCFELPRITIPDNYTTEVAENGQGYKSHMTYRLAKTEPKIFRY----- 111
DB 85 --SCVFSKGTSTIMKRYVITVAINQMGISSSDPLYVHTYIVVEPPPNLTLLEKHPED 142
QY 112 -KPVGIKMIQIEWIKPELAVSSD--LKYTEPRVTNSTMWENVNFAKRNKQNTY 167
DB 143 KPEYLMIK-----MSPTMTDVKSGWFIQYIRIKPEKAYDW-ETHTTL-----KOTOL 191
QY 168 NLGLOPFTFVYIALCAVSKESKFWSDSQE 198
DB 192 KIFNLVPGQKVLVQIRCK-PDHGYWSEWSPE 221

RESULT 10
PRLR_RAT STANDARD; PRT; 610 AA.
ID P05710; 062832; 063451; 063479; 063723; 064274;
AC P05710; 062832; 063451; 063479; 063723; 064274;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (Lactogen receptor).
PRLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_Taxid=10116;
RN [1]

```


RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91155946; PubMed=2293022;
 RA Shirota M., Banville D., Ali S., Jolicoeur C., Boutin J.M.,
 RA Ederly M., Djiane J., Kelly P.A.;
 RT "Expression of two forms of prolactin receptor in rat ovary and
 RT liver";
 RL Mol. Endocrinol. 4:1136-1143(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=90241201; PubMed=2159291;
 RA Zhang R., Buckko B., Tsai-Morris C.-H., Hu Z.Z., Dufau M.L.;
 RT "Isolation and characterization of two novel rat ovarian lactogen
 RT receptor cDNA species";
 RL Biochem. Biophys. Res. Commun. 168:415-422(1990).
 RN [3]
 RP SEQUENCE OF 281-610 FROM N.A.
 RA Banville D., Stocco R., Murphy K.K., Boie Y., Kelly P.A.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=88165059; PubMed=2832068;
 RA Boutin J.-M., Jolicoeur C., Okamura H., Gagnon J., Ederly M.,
 RA Shirota M., Banville D., Dusanter-Fourt I., Djiane J., Kelly P.A.;
 RT "Cloning and expression of the rat prolactin receptor, a member of
 RT the growth hormone/prolactin receptor gene family";
 RL Cell 53:69-77(1988).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Lymphoma;
 RX MEDLINE=92041834; PubMed=1718958;
 RA Ali S., Pelligrini I., Kelly P.A.;
 RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form
 RT of prolactin receptor";
 RL J. Biol. Chem. 266:20110-20117(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RX MEDLINE=95014432; PubMed=7929319;
 RA O'Neal K.D., Yu-Lee L.Y.;
 RT "Differential signal transduction of the short, Nb2, and long
 RT prolactin receptors. Activation of interferon regulatory factor-1 and
 RT cell proliferation";
 RL J. Biol. Chem. 269:26076-26082(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Long;
 CC IsoId=P05710-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=P05710-2; Sequence=VSP_001725, VSP_001726;
 CC Name=3; Synonyms=Medium;
 CC IsoId=P05710-3; Sequence=VSP_001727, VSP_001728;
 CC Name=4; Synonyms=NB2;
 CC IsoId=P05710-4; Sequence=VSP_001729;
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M57668; AAA41938.1; -
 CC EMBL; M34083; AAA79273.1; -
 CC EMBL; I48060; AAA79274.1; -
 CC EMBL; U34730; AAA2053.1; -
 CC EMBL; M19304; AAA41937.1; -
 CC DR

DR EMBL; M74152; AAA41946.1; -
 DR EMBL; U07567; AAA61784.1; -
 DR PIR; A29884; A29884.
 DR PIR; A34631; A34631.
 DR PIR; A36116; A36116.
 DR PIR; A41070; A41070.
 DR PIR; B34631; B34631.
 DR PDB; 1FEF; 20-DEC-00.
 DR InterPro; IPR002396; CR1A.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003528; Hemtopoetn_L_F1.
 DR Pfam; PF00041; FN3; 2.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS01352; HEMATOPO. REC. L F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
 KW Alternative splicing; 3D-structure.
 FT SIGNAL 1
 FT CHAIN 19
 FT DOMAIN 20 610
 FT TRANSMEM 20 229
 FT DOMAIN 230 253
 FT DOMAIN 254 610
 FT DOMAIN 20 117
 FT DOMAIN 119 222
 FT DISULFID 31 41
 FT DISULFID 70 81
 FT CARBOHYD 54 54
 FT CARBOHYD 99 99
 FT CARBOHYD 127 127
 FT VARSPLIC 131 150
 FT VARSPLIC 151 610
 FT VARSPLIC 281 310
 FT VARSPLIC 311 610
 FT VARSPLIC 342 539
 FT CONFLICT 236 236
 FT CONFLICT 345 345
 FT CONFLICT 465 465
 FT CONFLICT 466 466
 FT CONFLICT 469 469
 FT CONFLICT 541 541
 FT CONFLICT 555 555
 SQ SEQUENCE 610 AA; 68599 MW; 83D04D832861295D CRC64;
 Query Match 16.1%; Score 181; DB 1; Length 610;
 Best Local Similarity 27.9%; Pred. No. 2.8e-09;
 Matches 57; Conservative 35; Mismatches 94; Indels 18; Gaps 10;
 QY 3 PAKPENISCVYYRRNLTCTWSPGKETS-YTQYVKTAY-A-FGEKMD-NCTNSTSENK 59
 DB 23 PCKPEIHRCRSPDKRTFCWMNPGTDGGLPNYVS--TYSKGEKTYTECPDYSKGN- 79
 QY 60 ASCSFFLRITPDNYTEVAENDGVYKSHMTYRLENLAKTPPK--IFRYKPVYGI 117
 DB 80 -SCFSSKOYTSIMKIYITVNATQMGSSSDPLVDVYIVPEPPNLTLEVAQLDK 138
 QY 118 KMIQIEMIKPELAPVSS--DLKTYLFRFVNSTSNMENVNPAKRXKXKQNYNLGLOP 174
 DB 139 KTYLWKKSPPIITDVYKGMFMFEIRLKEBEAEW-EIHFTGHQTO---FKVFDLYP 193
 QY 175 FTEYVIALCAVAKESKESKFWSDWSOE 198
 DB 194 GQKYLIVQTRCK-PDHGYWRSWSOE 216
 RESULT 11
 PRIR CHICK STANDARD; PRT; 831 AA.

AC 004594;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (CPRLP).
 GN PRLR.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Kidney;
 RX MEDLINE=93075121; PubMed=1445292;
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
 RT "Double antenna structure of chicken prolactin receptor deduced from
 the cDNA sequence.";
 RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL: D13154; BAA02439.1; -;
 DR PIR: J01655; J01655.
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003528; Hemopoptn_L_F1.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 DR Fw Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT TRANSMEM 24 438
 FT DOMAIN 439 459
 FT DOMAIN 460 831
 FT DOMAIN 25 122
 FT DOMAIN 123 225
 FT DOMAIN 325 325
 FT DOMAIN 326 428
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 262 262
 FT CARBOHYD 303 303
 FT CARBOHYD 315 315
 FT CARBOHYD 335 335
 SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADB9 CRC64;
 Query Match 16.0%; Score 179.5; DB 1; Length 831;
 Best Local Similarity 26.7%; Pred. No. 5.7e-09;
 Matches 54; Conservative 26; Mismatches 109; Indels 13; Gaps 5;
 QY 3 PAKPENISCYYYRKNLTCTWSPKETS-Y-TQTVKRTVAFGEKHNCTNSSTSEKRS 61
 DB 231 PEKPTIKKRSPEKEFTCWKPGDLGHPNTYLLYSKEGBOVYECPDYRTAGRN--S 288

QY 62 CSFFFLPRTIPDNYTIEVANGDGVKSHMTYMLENIATKEPP--KIFRVKPVLGIR 119
 DB 289 CFEDDKHTSFMTITNTVATNEMGNSSDPHYVDTYIVQDDPPNVTLEKKPINRKP 348
 QY 120 MQIEWIKKELAPVSS--DLKTYLRFRTVNSTSMVEVNFAPAKRDKNOTYLTGLQPT 176
 DB 349 YVLTWSPPLADVSGWLTLEYELRLKPEBGEWETTFVGQOTQ-----YKQFSLNPK 403
 QY 177 EYVIALRCVAKESKFWSDMSOE 198
 DB 404 KTIQIHCKPDHGSSEWSS 425
 RESULT 12
 PRLR_MELGA STANDARD; PRT; 831 AA.
 AC 091094; Q91091; Q91092;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (TPRLR).
 GN PRLR.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagridae.
 NC NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97057891; PubMed=8902221;
 RA Zhou J.F., Zadoworny D., Guenene D., Kuhnlein U.;
 RT "Molecular cloning, tissue distribution, and expression of the
 prolactin receptor during various reproductive states in Meleagris
 gallopavo.";
 RT Gall. Reprod. 55:1081-1090(1996).
 RL [2]
 RN SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RP TISSUE=Ovary;
 RA Pites G.R., You S.K., Foster D.N., el Halawani M.E.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DDSI databases.
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 4 fibronectin type III domains.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L76587; AAB01544.1; -;
 DR EMBL: U22947; AAB05038.1; -;
 DR EMBL: U22924; AAB75039.1; -;
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003528; Hemopoptn_L_F1.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 DR Fw Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT TRANSMEM 24 438
 FT TRANSMEM 439 459
 FT DOMAIN 460 831
 FT DOMAIN 25 122
 FT DOMAIN 123 225
 FT DOMAIN 228 325
 FT CYTOPLASMIC (POTENTIAL).
 FT FIBRONECTIN TYPE-III 1.
 FT FIBRONECTIN TYPE-III 2.
 FT FIBRONECTIN TYPE-III 3.

FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
 FT DISULFID 36 46 BY SIMILARITY.
 FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 831 AA; 94394 MW; 22091632077FAC1 CRC64;
 Query Match 15.7%; Score 176.5; DB 1; Length 831;
 Best Local Similarity 26.2%; Pred. No. 1.1e-08;
 Matches 53; Conservative 26; Mismatches 110; Indels 13; Gaps 5;
 QY 3 PAKPENISCVYYRRKLTCTWSPGKETS-TOYVKTATYAFGRKNDCTTSSSENRA 61
 DB 231 PEKPTITKCRSPEKEFTCMWKGGLDGHPTVTLTYSKEGEQVYECDFRTAGPN--S 268
 QY 62 GSFPLPRITIPDNTIEVAENGDDGVYKSHMTYRLNIAKTEPK--IFRYKPVLGIR 119
 DB 289 CYFDKHTSFMTVYNTYVATNEMGSSDPHYDVTYIVDPDPANVTLEKPKINRKP 348
 QY 120 MIOIEMIKPELAPVSS--DLKYTLRFRTVNSTSWMEVPAKRNKDKNTYNLGLQPT 176
 DB 349 YLMLTWSPPLADVNSGMLTLDYELKPEEGEMETVVGQQTQ-----YKMFSLNPK 403
 QY 177 EYVIALRCVAKESKFWSDWSOE 198
 DB 404 KYIVQHCXKPDHHSSEWSSE 425
 RESULT 13
 ID 112S MOUSE STANDARD; PRT; 874 AA.
 AC P97378;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-12 receptor beta-2 chain precursor (IL-12 receptor beta-2) (IL-12R-beta2).
 GN IL12RB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97098510; PubMed=8943050;
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y., Gately M.K., Gubler U.;
 RT "A functional interleukin 12 receptor complex is composed of two beta-type cytokine receptor subunits";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007(1996).
 CC - FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A LOW AFFINITY.
 CC - SUBUNIT: DISULFIDE-LINKED HOMODIMER/OLIGOMER. THE FUNCTIONAL HIGH AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND IL12RB2.
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC - SIMILARITY: Contains 4 fibronectin type III domains.
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CC EMBL; U64199; AAB36676.1; -
 DR MGI; 1270861; 1112rb2.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003529; Hemtopopen_L_F2.
 DR Pfam; PF00041; fn3; 4.
 DR SMART; SMO0060; FN3; 4.
 DR ProSITE; PS01353; HEMATOPO. REC. L. F2; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 20 OR 23 (POTENTIAL).
 FT CHAIN 1 874 INTERLEUKIN-12 RECEPTOR BETA-2 CHAIN.
 FT DOMAIN 21 639 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 640 656 POTENTIAL.
 FT DOMAIN 657 874 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 137 230 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 240 322 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 436 523 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 534 622 FIBRONECTIN TYPE-III 4.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 112 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 874 AA; 98196 MW; 582E4D21B1FBD67 CRC64;
 Query Match 15.6%; Score 174.5; DB 1; Length 874;
 Best Local Similarity 30.8%; Pred. No. 1.1e-08;
 Matches 66; Conservative 31; Mismatches 96; Indels 21; Gaps 11;
 QY 3 PAKPENISCVYYRR-NLCTWSPGKETS-TOYVKTATYAFGRKNDCTTSSSENRA 60
 DB 137 PEKPTITKCRSPEKEFTCMWKGGLDGHPTVTLTYSKEGEQVYECDFRTAGPN--S 268
 QY 62 GSFPLPRITIPDNTIEVAENGDDGVYKSHMTYRLNIAKTEPK--IFRYKPVLGIR 119
 DB 289 CYFDKHTSFMTVYNTYVATNEMGSSDPHYDVTYIVDPDPANVTLEKPKINRKP 348
 QY 120 MIOIEMIKPELAPVSS--DLKYTLRFRTVNSTSWMEVPAKRNKDKNTYNLGLQPT 176
 DB 349 YLMLTWSPPLADVNSGMLTLDYELKPEEGEMETVVGQQTQ-----YKMFSLNPK 403
 QY 177 EYVIALRCVAKESKFWSDWSOE 198
 DB 404 KYIVQHCXKPDHHSSEWSSE 425
 RESULT 14
 ID PRIR_RABIT STANDARD; PRT; 616 AA.
 AC P14787;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Prolactin receptor precursor (PR-L-R).
 GN PR-LR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Mammary gland;
 MEDLINE=89184578; PubMed=2928321;

RA Edey M., Jolicoeur C., Levi-Meyrueis C., Dusanter-Fourt I.,
 RA Peticidou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;
 RA "Identification and sequence analysis of a second form of prolactin
 RT receptor by molecular cloning of complementary DNA from rabbit
 RT mammary gland."; *Proc. Natl. Acad. Sci. U.S.A.* 86:2112-2116(1989).
 RN [2]
 RP 3D-STRUCTURE MODELING OF 30-228.
 RX MEDLINE=97248733; PubMed=9094747;
 RA Helaby D., Thoreau E., Djiane J., Morron J.-P.;
 RT "homology" modeling of rabbit prolactin hormone complexed with its
 RT receptor."; *Protein* 27:459-468(1997).
 RL Proteins 27:459-468(1997).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -----
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 CC -----
 CC EMBL: J04510; AAA31457.1; -.
 DR PIR: A30304; A30304.
 DR PDB: 1AN3; 03-DEC-97.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR003528; Hemicoptn_L_F1.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS0135; HEMITOPD_REC_L_F1; 1.
 DR PROSITE: PS0135; Glycoprotein; Signal; Repeat; 3D-structure.
 DR RecProt: Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
 FT STGNL 1 24
 FT CHAIN 25 616
 FT DOMAIN 25 234
 FT TRANSLEM 235 258
 FT DOMAIN 259 616
 FT DOMAIN 122 122
 FT DOMAIN 124 227
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 86
 FT CARBOHYD 104 104
 FT CARBOHYD 132 132
 FT STRAND 36 38
 FT STRAND 44 46
 FT STRAND 50 50
 FT STRAND 55 55
 FT STRAND 61 65
 FT STRAND 73 74
 FT STRAND 77 77
 FT TURN 83 84
 FT TURN 86 88
 FT STRAND 91 92
 FT TURN 98 104
 FT TURN 109 110
 FT STRAND 118 120
 FT TURN 121 124
 FT STRAND 125 125
 FT STRAND 131 137
 FT STRAND 147 152
 FT TURN 160 161
 FT STRAND 167 174
 FT STRAND 181 182
 FT STRAND 186 186
 FT STRAND 190 193
 FT TURN 198 199
 FT STRAND 202

FT STRAND 222 223
 SQ SEQUENCE 616 AA; 68840 MW; 800E316FEFF7108C CRC64;
 Query Match 15.1%; Score 169; DB 1; Length 616;
 Best Local Similarity 29.3%; Pred. No. 3, 7e-08; Indels 20; Gaps 11;
 Matches 60; Conservative 27; Mismatches 98;
 QY 3 PAKPENISCVYYRKNLTCTWSPGKETSY-TQYVARY-ARGE-KHNDCTNSSTSEN 58
 DB 28 PCKRPFIFKRSPEKEFTCWMPRGADGILPTVTL--TYHKGFTITHE-CPDYKCGPN 84
 QY 59 RASCSFFLPRTIPDNYITEVAENGQVYKSHMTYRLNIAKTEPP-KIFRYKPVLG 116
 DB 85 --SCYFSKKHSTSIWTYIITVNATQMGSSVSDPRVDYTVIEPDPVNLTLVGHPEP 142
 QY 117 IKRMIOIEMIKPELAPVSS---DLKYLRFRTVNSWMEVFAKRRKDKQNTYNTGLQ 173
 DB 143 RKPYLWVKWLPPLTLVDVRSGLTLQYETILKPEKAEW-ETHPA---GQQTQFKILSLY 197
 QY 174 PFTEVYIALRCVAKSKFWSWDSOE 198
 DB 198 PGKXIVQVRCK-PDHGFWSWSPE 221
 RESULT 15
 ID GCSR HUMAN STANDARD; PRT; 836 AA.
 AC 099062;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-FEB-2003 (Rel. 42, Last annotation update)
 DE Granulocyte colony stimulating factor receptor precursor (G-CSF-R)
 DE (CD114 antigen).
 GN CSF3R OR GCSFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=91079757; PubMed=2147944;
 RA Larsen A., Davis T., Curtis B.M., Gimpel S., Sims J.E., Cosman D.,
 RA Park L., Sorensen E., March C.J., Smith C.A.;
 RT "Expression cloning of a human granulocyte colony-stimulating factor
 RT receptor: a structural mosaic of hematopoietic receptor,
 RT immunoglobulin, and fibronectin domains."; *J. Exp. Med.* 172:1559-1570(1990).
 RL J. Exp. Med. 172:1559-1570(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=91062348; PubMed=1701053;
 RA Fukunaga R., Seto Y., Mizushima S., Nagata S.;
 RT "Three different mRNAs encoding human granulocyte colony-stimulating
 RT factor receptor."; *Proc. Natl. Acad. Sci. U.S.A.* 87:8702-8706(1990).
 RL J. Immunol. 148:259-266(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92091782; PubMed=1530796;
 RA Seto Y., Fukunaga R., Nagata S.;
 RT "Chromosomal gene organization of the human granulocyte colony-
 RT stimulating factor receptor."; *J. Immunol.* 148:259-266(1992).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS THR-231; ASN-320; ARG-346; LYS-405;
 RP GLN-440; HIS-510; HIS-562 AND CYS-583.
 RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (SEP-2002) to the EMBL/Genbank/DDJ databases.
 RN [5]
 RP DOMAINS STRUCTURE.
 RX MEDLINE=92007729; PubMed=1717255;
 RA Fukunaga R., Ishizaka-Ikeda E., Pan C.-X., Seto Y., Nagata S.;

RT "Functional domains of the granulocyte colony-stimulating factor
RT receptor."; EMO J. 10:2855-2865(1991).
RL [6]
RN DISEASE.
RP MEDLINE=94240159; PubMed=7514305;
RX Dong F., Hoefsloot L.H., Scheijen A.M., Broeders C.A., Meijer Y.,
RA Veerman A.J., Touw I.P., Lowenberg B.;
RT "Identification of a nonsense mutation in the granulocyte-colony-
RT stimulating factor receptor in severe congenital neutropenia.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4480-4484(1994).
RN [7]
RP STRUCTURE BY NMR OF 227-334.
RX MEDLINE=97331327; PubMed=18167559;
RA Yamasaki K., Naito S., Aneguchi H., Ohkubo T., Ota Y.;
RT "Solution structure of an extracellular domain containing the WSXWS
RT motif of the granulocyte colony-stimulating factor receptor and its
RT interaction with ligand.";
RL Nat. Struct. Biol. 4:498-503(1997).
RN [8]
RP 3D-STRUCTURE MODELING OF 125-331.
RX MEDLINE=98037802; PubMed=9368043;
RA Layton J.E., Iaria J., Smith D.K., Treutlein H.R.;
RT "Identification of a ligand-binding site on the granulocyte colony-
RT stimulating factor receptor by molecular modelling and mutagenesis.";
RL J. Biol. Chem. 272:29735-29741(1997).
CC -1- FUNCTION: RECEPTOR FOR GRANULOCYTE COLONY-STIMULATING FACTOR (G-
CC CSF). IN ADDITION IT MAY FUNCTION IN SOME ADHESION OR RECOGNITION
CC EVENTS AT THE CELL SURFACE.
CC -1- SUBUNIT: DIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE GCSFR-2 FORM,
CC WHICH LACKS THE TRANSMEMBRANE DOMAIN, MAY REPRESENT A SOLUBLE FORM
CC OF THE RECEPTOR.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Additional isoforms seem to exist. Experimental
CC confirmation may be lacking for some isoforms;
CC Name=1; Synonyms=GCSFR-1;
CC IsoId=Q99062-1; Sequence=Displayed;
CC Name=2; Synonyms=GCSFR-2;
CC IsoId=Q99062-2; Sequence=VSP_001674;
CC Name=3; Synonyms=GCSFR-3;
CC IsoId=Q99062-3; Sequence=VSP_001673;
CC Name=4; Synonyms=GCSFR-4, D7;
CC IsoId=Q99062-4; Sequence=VSP_001671, VSP_001672;
CC -1- TISSUE SPECIFICITY: ONE OR SEVERAL FORMS HAVE BEEN FOUND IN
CC MYELOGENOUS LEUKEMIA CELL LINE KG-1, LEUKEMIA U937 CELL LINE, IN
CC BONE MARROW CELLS, PLACENTA, AND PERIPHERAL BLOOD GRANULOCYTES.
CC THE GCSFR-2 FORM HAS BEEN FOUND ONLY IN LEUKEMIA U937 CELLS. THE
CC GCSFR-3 FORM IS HIGHLY EXPRESSED IN PLACENTA.
CC -1- DISEASE: Defects in CSFR3 might be a cause of severe congenital
CC neutropenia (SCN) in some patients.
CC -1- SIMILARITY: Contains 5 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD114 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd114.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X55721; CAA39253.1; -
DR EMBL; X55720; CAA39252.1; -
DR EMBL; S71484; AAB20660.1; -
DR EMBL; M59818; AAA63176.1; -
DR EMBL; M59819; AAA63177.1; -
DR EMBL; M59820; AAA63178.1; -
DR EMBL; AY148100; AAN05790.1; -

DR	P1R:	B38252;	B38252.
DR	P1R:	C38252;	C38252.
DR	P1R:	JH0329;	JH0329.
DR	PDS:	IAT7;	28-JAN-98.
DR	Genew:	HGNC:2439;	CSFAR.
DR	MIM:	138971;	-.
DR	GO:	GO:0005887;	C:integral to plasma membrane; TAS.
DR	GO:	GO:0004872;	F:receptor activity; TAS.
DR	GO:	GO:0006952;	F:defence response; TAS.
DR	InterPro:	IPR002996;	CRIA.
DR	InterPro:	IPR003961;	FN III.
DR	InterPro:	IPR003529;	Hemtopoptn_L_F2.
DR	Pfam:	PF00041;	fntj_3.
DR	SMART:	SM00060;	FN3_2.
DR	PROSITE:	PS01353;	HEMATOPO_REC_L_F2; 1.
KW	Cell adhesion;	Receptor;	Repeat; Signal; Transmembrane;
KW	Immunoglobulin domain;	Glycoprotein;	Alternative splicing;
KW	Polymorphism;	3D-structure.	
FT	SIGNAL	1	24
FT	CHAIN	25	836
FT			
FT	DOMAIN	25	627
FT	TRANSEM	628	650
FT	DOMAIN	651	836
FT	DOMAIN	25	117
FT	DOMAIN	121	227
FT	DOMAIN	228	332
FT	DOMAIN	333	428
FT	DOMAIN	429	525
FT	DOMAIN	526	621
FT	DISULFID	131	142
FT	DISULFID	248	295
FT	DISULFID	266	309
FT	CARBOHYD	51	51
FT	CARBOHYD	93	93
FT	CARBOHYD	128	128
FT	CARBOHYD	134	134
FT	CARBOHYD	389	389
FT	CARBOHYD	474	474
FT	CARBOHYD	579	579
FT	CARBOHYD	610	610
FT	VASPLIC	750	783
FT			
FT			
FT	VASPLIC	784	836
FT			
FT	VASPLIC	680	680
FT			
FT	VARSPLIC	622	836
FT			
FT			
FT	VARIANT	231	231
FT			
FT	VARIANT	320	320
FT			
FT	VARIANT	346	346
FT			
FT	VARIANT	405	405
FT			
FT	VARIANT	440	440
FT			
FT	VARIANT	510	510
FT			

FT VARIANT 562 562 Y -> H.
FT VARIANT 583 583 /FTId=VAR_014331.
FT STRAND 127 133 R -> C.
FT TURN 135 136 /FTId=VAR_014332.
FT STRAND 140 145

Query Match 14.8%; Score 166; DB 1; Length 836;
Best Local Similarity 27.1%; Pred. No. 1e-07;
Matches 64; Conservative 22; Mismatches 96; Indels 54; Gaps 10;

QY 3 PAKPENISCVYYRKNLT-----CTWSPGKETS-TOYTVKRTYAFGEKHNDCTNSST- 55
DB 123 PAIPHNLSCL-----MNLTSLSLCQWEPGPETHLPSTFLKSPKSRG---NCOTQDST 174
QY 56 -----SENBASCSFELPRITIPNDYITEVAENGSGVYKSHMTYWRLENIAKTEPPKIFR 110
DB 175 LDCVPKDGQSHCCIPRHLLLYQNMGIWQAEENALGTSMSPOLCLDPMDVVKLEPPMLRT 234
QY 111 VKPVLGIKRMIOIEWIKPELAPVSS-----DLKYTLRFRTV-NSTSWME 153
DB 235 MDP-----SPEAAPQAGCLQLCWEPWQGLHINQKCELRHKPQGEASWAL 281
QY 154 VNFAPKRNKDNQYNTLTGLOPTEYVIALRC-AVKESKFWSDWSQEKMGTEEEAP 208
DB 282 VG---PLPLEALQYELGGLPATAYTLQIRCIHWPLFGHWSWSPSLERLTERAP 334

Search completed: August 18, 2003, 13:27:39
Job time : 16.81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:47 ; Search time 73.6152 Seconds
(without alignments)
729.128 Million cell updates/sec

Title: US-09-892-949-2_COPY_20_227

Perfect score: 1121
Sequence: 1 ALPAPENISCVYRRKNTL.....SKFMSDWSQEKMGTEBAP 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs., 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP_ARCHAEA:*
- 2: SP_BACTERIA:*
- 3: SP_FUNGI:*
- 4: SP_HUMAN:*
- 5: SP_INVERTEBRATE:*
- 6: SP_MAMMAL:*
- 7: SP_MHC:*
- 8: SP_ORGANELLE:*
- 9: SP_PHAGE:*
- 10: SP_PLANT:*
- 11: SP_RODENT:*
- 12: SP_VIRUS:*
- 13: SP_VERTEBRATE:*
- 14: SP_UNCLASSIFIED:*
- 15: SP_VIRUS:*
- 16: SP_BACTERIAP:*
- 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1121	100.0	509	4 Q8WYJ0	Q8WYJ0 homo sapien
2	1121	100.0	732	4 Q8N117	Q8N117 homo sapien
3	502.5	44.8	716	11 Q8K5B1	Q8K5B1 mus musculu
4	502.5	44.8	716	11 Q8K5B1	Q8K5B1 mus musculu
5	287	25.6	881	13 Q57519	Q57519 xenopus lae
6	278	24.8	918	13 Q9W6U9	Q9W6U9 gallus gall
7	231	20.6	422	4 Q9UH5	Q9UH5 homo sapien
8	231	20.6	422	4 Q75462	Q75462 homo sapien
9	229	20.4	425	11 Q9UM58	Q9UM58 mus musculu
10	209	18.6	861	6 Q9BEG2	Q9BEG2 bos taurus
11	204	18.2	710	13 Q57520	Q57520 xenopus lae
12	203	18.1	848	6 Q8WNT4	Q8WNT4 sus scrofa
13	198	17.7	861	6 Q8WNT4	Q8WNT4 sus scrofa
14	194	17.3	292	11 Q8C7G1	Q8C7G1 mus musculu
15	191	17.0	608	11 Q9J0Z1	Q9J0Z1 mus musculu
16	178.5	15.9	626	13 Q9W0G7	Q9W0G7 cynops pyr

17	172.5	15.4	604	13 Q8Q554	Q8Q554 cyprinus ca
18	172	15.3	622	6 Q9GLW3	Q9GLW3 ursus marit
19	169	15.1	627	6 Q9N0J7	Q9N0J7 callithrix
20	165.5	14.8	611	13 Q9PT9	Q9PT9 xenopus lae
21	162	14.5	644	11 Q8K4B4	Q8K4B4 mus musculu
22	160	14.3	629	4 Q8WFO9	Q8WFO9 mus musculu
23	158.5	14.1	1093	11 Q70535	Q70535 ratu
24	156	13.9	383	11 Q8H786	Q8H786 mus musculu
25	156	13.9	385	11 Q8VHK6	Q8VHK6 ratu
26	154.5	13.8	600	13 Q9PT9	Q9PT9 carassius a
27	154	13.7	345	13 Q93404	Q93404 oreochromis
28	154	13.7	625	6 Q9XS92	Q9XS92 trichosturus
29	153.5	13.7	424	11 Q8C123	Q8C123 mus musculu
30	153	13.6	206	4 Q16354	Q16354 homo sapien
31	153	13.6	268	4 Q8TD78	Q8TD78 homo sapien
32	153	13.6	288	4 Q96P36	Q96P36 homo sapien
33	153	13.6	349	4 Q9UH5	Q9UH5 homo sapien
34	153	13.6	376	4 Q96P35	Q96P35 homo sapien
35	151.5	13.5	212	13 Q8JFT3	Q8JFT3 brachydanto
36	149.5	13.3	424	11 Q8BNM4	Q8BNM4 mus musculu
37	148.5	13.2	611	13 Q9IBP6	Q9IBP6 xenopus lae
38	148.5	13.2	611	13 Q9PT9	Q9PT9 xenopus lae
39	146.5	13.1	372	11 Q8H507	Q8H507 mus musculu
40	146.5	13.1	432	11 P70225	P70225 mus musculu
41	145	12.9	217	6 Q46386	Q46386 mustela vis
42	144	12.8	109	6 Q8SPV0	Q8SPV0 canis fami
43	142	12.7	422	4 Q16542	Q16542 homo sapien
44	141.5	12.6	636	13 Q90Z16	Q90Z16 parailichthy
45	140.5	12.5	432	11 Q64385	Q64385 mus musculu

ALIGNMENTS

RESULT 1	Q8WYJ0	PRELIMINARY	PRT	509 AA.
AC	Q8WYJ0			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	CRL3 protein.			
GN	CRL3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zhang W., Wan T., He L., Yuan Z., Cao X.;			
RT	"A novel soluble type I cytokine receptor."			
RL	Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF106913; AAL36452.1; ..			
DR	InterPro; IPR002996; CRLA.			
DR	InterPro; IPR003961; FN_III.			
DR	Pfam; PF00041; fn3; 2.			
DR	SMART; SM00060; FN3; 3.			
SO	SEQUENCE 509 AA; 58390 MW; 5DC85C59E170D4B CRC64;			
Query Match	100.0%; Score 1121; DB 4; Length 509;			
Best Local Similarity	100.0%; Pred. No. 5,56-98;			
Matches 208; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 ALPAPENISCVYRRKNTLCTWSGKETSQYTVKRTYVAGEGHDNCTNSSENRA 60			Q8G54 cyprinus ca
QY	33 ALPAPENISCVYRRKNTLCTWSGKETSQYTVKRTYVAGEGHDNCTNSSENRA 92			Q9GLW3 ursus marit
QY	61 SCSPFLPRTTIPDNTTIEVEAENGGVKSHMTYRLLENIAKTEBPXIFRVVPGVIGIRM 120			Q9N0J7 callithrix
QY	93 SCSPFLPRTTIPDNTTIEVEAENGGVKSHMTYRLLENIAKTEBPXIFRVVPGVIGIRM 152			Q9PT9 xenopus lae
QY	121 IOENIKPELAVSSDLKTYTLRFTVNSTSWMEVFAKORXKQNTYNTLGQPTETVYI 180			Q8K4B4 mus musculu

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Db 153 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFAPKRNKDQNTYNTGLQPTFEYVI 212
Qy 181 ALRCAYESKFSKFSMDMSQEKMGTEBEAP 208
Db 213 ALRCAYESKFSKFSMDMSQEKMGTEBEAP 240

RESULT 2
Q8N117 PRELIMINARY; PRT; 732 AA.
AC Q8N117;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gp130-like monocyte receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21986187; PubMed=11877449;
RA Chillard N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals
RT Proliferation, and Activates STAT-3 and STAT-5."
RL J. Biol. Chem. 277:16831-16836 (2002).
DR EMBL; AF486620; AA027958.1; -
DR InterPro; IPR002996; CRA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; FN3; 1.
DR SMART; SM00060; FN3; 3.
KW Receptor.
SQ SEQUENCE 732 AA; 82953 MW; 30F84BD3D99A20E CRC64;

Query Match 100.0%; Score 1121; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 8.7e-98;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALPAKPNISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 60
Db 20 ALPAKPNISCVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 79
Qy 61 SCGFPLPRITIPDNYTTEVEAENGQGVKSHMTYRWLENIATKEPPKIFRYKPVLGIR 120
Db 80 SCGFPLPRITIPDNYTTEVEAENGQGVKSHMTYRWLENIATKEPPKIFRYKPVLGIR 139
Qy 121 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFAPKRNKDQNTYNTGLQPTFEYVI 180
Db 140 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFAPKRNKDQNTYNTGLQPTFEYVI 199
Qy 181 ALRCAYESKFSKFSMDMSQEKMGTEBEAP 208
Db 200 ALRCAYESKFSKFSMDMSQEKMGTEBEAP 227

RESULT 3
Q8K5B1 PRELIMINARY; PRT; 716 AA.
AC Q8K5B1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gp130-like monocyte receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21986187; PubMed=11877449;
RA Chillard N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals
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RT Proliferation, and Activates STAT-3 and STAT-5."
RL J. Biol. Chem. 277:16831-16836 (2002).
DR EMBL; AF486621; AA027959.1; -
DR MGD; MGI:2180511; Glimr.
DR InterPro; IPR002996; CRA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; FN3; 1.
DR SMART; SM00060; FN3; 3.
KW Receptor.
SQ SEQUENCE 716 AA; 80641 MW; 39E6B0B253F7C7E5 CRC64;

Query Match 44.8%; Score 502.5; DB 11; Length 716;
Best Local Similarity 49.8%; Pred. No. 4.1e-39;
Matches 104; Conservative 29; Mismatches 59; Indels 17; Gaps 5;

Qy 2 LPKAPNISCYVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 61
Db 20 LPKAPNISCYVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 71
Qy 62 SCGFPLPRITIPDNYTTEVEAENGQGVKSHMTYRWLENIATKEPPKIFRYKPVLGIR 119
Db 72 ASYSPFRSCAMPDICSVEVQKNGDGKYSIDITYMHLISIAKTEPPILSVNP1--CNR 129
Qy 120 IQIEWIKPELAPVSSDLKTYLRFRVTNSTSMWEVNFAPKRNKDQNTYNTGLQPTFEYVI 179
Db 130 MFOIQW-KPREKTRGPFVCMRLFRVTNSRWTEVNF---ENCKQVCNLTGLQAFTEYV 184
Qy 180 IALRCAYESKFSKFSMDMSQEKMGTEBEAP 208
Db 185 LALRFPRNDSRYMSKSKSEETRWTEVNP 213

RESULT 4
Q8R501 PRELIMINARY; PRT; 716 AA.
AC Q8R501;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Cytokine receptor NR10.
GN GIMR OR NR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
RT "Polymorphism between C57BL/6 and Balb/c in the novel cytokine
RT receptor NR10."
RL Submitted (Apr-2002) to the EMBL/Genbank/DDJ databases.
DR EMBL; AB083111; BAB88745.1; -
DR MGD; MGI:2180511; Glimr.
DR InterPro; IPR002996; CRA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; FN3; 1.
DR SMART; SM00060; FN3; 3.
KW Receptor.
SQ SEQUENCE 716 AA; 80598 MW; CBF718DCCD40FC7 CRC64;

Query Match 44.8%; Score 502.5; DB 11; Length 716;
Best Local Similarity 49.8%; Pred. No. 4.1e-39;
Matches 104; Conservative 29; Mismatches 59; Indels 17; Gaps 5;

Qy 2 LPKAPNISCYVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 61
Db 20 LPKAPNISCYVYYRNKLTCTWSPGKETSQYQYVRYAFAFGKDKDNTTNSSENRA 71
Qy 62 SCGFPLPRITIPDNYTTEVEAENGQGVKSHMTYRWLENIATKEPPKIFRYKPVLGIR 119
Db 72 ASYSPFRSCAMPDICSVEVQKNGDGKYSIDITYMHLISIAKTEPPILSVNP1--CNR 129
```


QY 120 MGIEMIKPELAPVSSDLKTYTLRFTVNSTSMVEVNFPAKRDKNQNTNLGLQPTTEVY 179
Db 130 MFOIOM-KPREKTRGFPVLCMLRFTVNSTSMVEVNF-----ENCKQVNCNLGLQPTTEVY 184
QY 180 IALRCAYKESKFWSDMSQKMGMTTEEAR 208
Db 185 IALRFRFNDSRYSKMSKEETVTEWEVP 213

RESULT 5

057519 PRELIMINARY; PRT; 881 AA.
AC 057519;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gp130p1.
GN XGp130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RT "Partial characterization of putative Xenopus gp130.";
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -.
DR HSSP; P40189; 180U.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hemtopoptn_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;

Query Match 25.6%; Score 287; DB 13; Length 881;
Best Local Similarity 33.0%; Pred. No. 1.5e-18;
Matches 69; Conservative 35; Mismatches 91; Indels 14; Gaps 6;

QY 3 PAKPENISCVYYRRKNLTCTWSPKETS-YQYVRYA-FGEKNDCTNSTSENKA 60
Db 122 PDKPTNLTCTVYVNDLCTWDPGRPTNLTPTVYLSHRAHFGAVYCRGANN----- 173
QY 61 SCSEFLPRTTIPDNTTIEVAENGCVITASHMTYRLKLEIATPEPKIRVKGVLGKSM 120
Db 174 SCTHSPGFQFYIDTTFQVEATNELGIQSEFLTIDPVNIVKPNPQISELSSLEPVA 233
QY 121 IGIEWIKPELAPVSSDLKTYTLRFTVNSTSMVEVNFPAKRDKNQNTNLGLQPTTEVY 180
Db 234 LKIEWKNP--ITNAFLKTNINIRPYKTDW--EMVPEEDTASHRDSFTLQDLIPNTVEV 290
QY 181 ALRCAYKESK-FWSDMSQKMGMTTEEAR 208
Db 291 SIRCIHKDGHGFWSDMSSELKQVTPPEAP 319

RESULT 6

09M6U9 PRELIMINARY; PRT; 918 AA.
AC 09M6U9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Glycoprotein 130 precursor.
GN Gp130.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic heart;
RX MEDLINE=99026068; PubMed=9806927;
RA Geiselen M., Heller S., Pennica D., Ernberger U., Rohrer H.;
RT "The specification of sympathetic neurotransmitter phenotype depends
on gp130 cytokine receptor signaling.";
RL Development 125:4791-4801(1998).
DR EMBL; AJ011688; CAB42084.1; -.
DR HSSP; P40189; 180U.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hemtopoptn_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 4.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW SIGNAL.
FT SIGNAL. 1 26 POTENTIAL.
SQ SEQUENCE 918 AA; 102495 MW; FE7625FF3E3613BF CRC64;

Query Match 24.8%; Score 278; DB 13; Length 918;
Best Local Similarity 27.7%; Pred. No. 1.1e-17;
Matches 64; Conservative 47; Mismatches 66; Indels 54; Gaps 9;

QY 3 PAKPENISCVYYRRKNLTCTWSPKETS-YQYVRYA-FGEKNDCTNSTSEN 58
Db 129 PEKPNLTCTVYVNDLCTWDPGRPTNLTPTVYLSHRAHFGAVYCRGANN----- 163
QY 59 RASCSEFLPRTTIPDNTTIEVAENGCVITASHMTYRLKLEIATPEPKIRVKGVLGKSM 98
Db 164 RFLRYKMPRETFPCIDPEYVNSCTISDVQFVNLVFWVAANALGAESDHLVFDPIE 223
QY 99 NIAKTEPKIRVYKVLGKSMIGIEWIKPELAPVSSDLKTYTLRFTVNSTSMVEVNFPAK 158
Db 224 -IVKPPPPRNLSVNSGT-LPVLKLSW-ENOISTYMLKTRIRIRISSDTNMEVP-DE 279
QY 159 NRKDNQNTNLGLQPTTEVYIALRCAYKES-KFWSMSQKMGMTTEEAR 208
Db 280 DTASPRTSFSIGLAPRYTEVYFIRCKMEDGVGFWSMSSEQIGVTTEDKP 330

RESULT 7

09UHNS PRELIMINARY; PRT; 422 AA.
AC 09UHNS;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Class I cytokine receptor.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jernberg A.C., Gilbert T., Whitmore T.E.,
Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RT Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0DC5F7A01B942EE CRC64;

Query Match 20.6%; Score 231; DB 4; Length 422;
Best Local Similarity 29.2%; Pred. No. 1.2e-13;
Matches 66; Conservative 34; Mismatches 90; Indels 36; Gaps 10;

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QY 3 PAKPENISCVYYRKNLTCTWSPGK--ET-SYQYTVKRTYAFGEKNDCTNNSSTSENK 59
DB 135 PEKPNVISCWSKMKDLCTCMTGAGHGETFLHTNYSLKTKLRWYGQDNTCEBYHTVGP 193
QY 60 ASC-----SFLPRITIPDNTYIEVEAENGDVISKSHMTYRLNIATKEPPKIRVXP 113
DB 194 -SCHIRKDLALFTF-----YEIWEATNRLGSARSDVLTLDLVVTTDPPDVHYSR 245
QY 114 VLGIKMIQIEWIKPELAPVSSDL---KYLRFRTVNSTSMWEVNFAPKRNKQNTYNL 169
DB 246 VGLLEDOQLSVRWSP---PALKDPLFOAKYQIRYVEDSDVMDKVVDDVSNQ-----TSCRL 298
QY 170 TGLQPFTEYVIALRC-----AVKSKFMSDMSQEKMGMT-BEAP 208
DB 299 AGLKPGTYFVQVRCNPFGIYSGKKAGIMSEWSHPTAASPERSER 344

RESULT 8
ID 075462 PRELIMINARY; PRT; 422 AA.
AC 075462;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytokine-like factor-1 precursor.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Grelener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Villbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-1 Receptor Family.";
RN 12
RN J. Immunol. 0:0-0(1998).
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hematopoietic cytokine receptor domain.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059293; AAC28335.1; -.
DR EMBL; AF073515; AAC39681.1; -.
DR HSSP; P16471; 1BP3.
DR GeneW; HGNC:2364; CRLL1.
DR InterPro; IPR002996; CRIL.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; IG_1like.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT SIGNAL 1 37
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9DFCB01B84228 CRC64;

Query Match 20.4%; Score 231; DB 4; Length 422;
Best Local Similarity 29.2%; Pred. No. 1.2e-13;
Matches 66; Conservative 34; Mismatches 90; Indels 36; Gaps 10;

QY 3 PAKPENISCVYYRKNLTCTWSPGK--ET-SYQYTVKRTYAFGEKNDCTNNSSTSENK 59
DB 135 PEKPNVISCWSKMKDLCTCMTGAGHGETFLHTNYSLKTKLRWYGQDNTCEBYHTVGP 193
QY 60 ASC-----SFLPRITIPDNTYIEVEAENGDVISKSHMTYRLNIATKEPPKIRVXP 113
DB 194 -SCHIRKDLALFTF-----YEIWEATNRLGSARSDVLTLDLVVTTDPPDVHYSR 245
QY 114 VLGIKMIQIEWIKPELAPVSSDL---KYLRFRTVNSTSMWEVNFAPKRNKQNTYNL 169
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DB 246 VGLLEDOQLSVRWSP---PALKDPLFOAKYQIRYVEDSDVMDKVVDDVSNQ-----TSCRL 298
QY 170 TGLQPFTEYVIALRC-----AVKSKFMSDMSQEKMGMT-BEAP 208
DB 299 AGLKPGTYFVQVRCNPFGIYSGKKAGIMSEWSHPTAASPERSER 344

RESULT 9
ID 09JMS8 PRELIMINARY; PRT; 425 AA.
AC 09JMS8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytokine receptor like molecule 3 precursor.
GN CRLL1 OR CRLL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN 11
RP SEQUENCE FROM N.A.
RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
RT "Cytokine receptor like molecule 3.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040038; BAA92777.1; -.
DR HSSP; P16471; 1BP3.
DR MGD; MGI:1340030; Crll1.
DR InterPro; IPR002996; CRIL.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
FT SIGNAL 1 34
FT CHAIN 35 425 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 20.4%; Score 229; DB 11; Length 425;
Best Local Similarity 29.2%; Pred. No. 1.9e-13;
Matches 66; Conservative 34; Mismatches 90; Indels 36; Gaps 10;

QY 3 PAKPENISCVYYRKNLTCTWSPGK--ET-SYQYTVKRTYAFGEKNDCTNNSSTSENK 59
DB 138 PEKPNVISCWSKMKDLCTCMTGAGHGETFLHTNYSLKTKLRWYGQDNTCEBYHTVGP 196
QY 60 ASC-----SFLPRITIPDNTYIEVEAENGDVISKSHMTYRLNIATKEPPKIRVXP 113
DB 197 -SCHIRKDLALFTF-----YEIWEATNRLGSARSDVLTLDLVVTTDPPDVHYSR 248
QY 114 VLGIKMIQIEWIKPELAPVSSDL---KYLRFRTVNSTSMWEVNFAPKRNKQNTYNL 169
DB 249 VGLLEDOQLSVRWSP---PALKDPLFOAKYQIRYVEDSDVMDKVVDDVSNQ-----TSCRL 301
QY 170 TGLQPFTEYVIALRC-----AVKSKFMSDMSQEKMGMT-BEAP 208
DB 302 AGLKPGTYFVQVRCNPFGIYSGKKAGIMSEWSHPTAASPERSER 347

RESULT 10
ID 09BEG2 PRELIMINARY; PRT; 861 AA.
AC 09BEG2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE IL-12 receptor beta2 precursor.
GN IL-12R BETA2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN 11
RP SEQUENCE FROM N.A.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RP Kohno T.;
RT "Cloning of porcine interleukin-12 receptor beta 2 gene,"
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF330213; AA047541.1; -
DR InterPro: IPR002896; CRIA.
DR InterPro: IPR003861; FN_III.
DR InterPro: IPR003529; Hemitopdom_L_F2.
DR Pfam: PF00041; fn3_3.
DR SMART: SM00060; FN3_4.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor.
SQ SEQUENCE 861 AA; 96055 MW; 2AB63B3C5CF42534 CRC64;

	Query Match	17.7%	Score 198;	DB 6;	Length 861;
	Best Local Similarity	30.0%	Pred. No. 4e-10;		
	Matches	64;	Conservative	32;	Mismatches 97;
				Indels	20; Gaps
OY	2 LPAKENTISCVYY-YRKNLTCTWSPGKETSYQYTVARKYAFGKHNCNTTSSTSE-	57			
Dd	: : : : : :	:	:	:	:
OY	123 VPEQFQNSSCMQGGEGTACSMWDGRDHTYTATLQLN--GPK-NLTWQKCSIDYY	177			
OY	58 -NRASCFFLPRIITPDNYTTEVEAENDGDVIKSHMTWRLENIKTBEPKIFRYKPIUG	116			
Dd	: : : : : :	:	:	:	:
OY	178 CSDLDLGINLPESSESSTMAOVTAINSIGTASSLPSTFTFLIDVRPLPMDIRIKCVA	237			
OY	117 IKRMIIEMIKBELAPVASDKCYTLRFRTVNSTSWMEVFANRNKKDKQTLYNLGLQEPFT	176			
Dd	: : : : : :	:	:	:	:
OY	238 SVSTCTLLQMBDEGLV-----LLNRLRYRPVYSRSNNMNV-AIMNAAGR---HDLVLKCFET	288			
OY	177 EYVIALRCAYKEK-FNSDWGSGEKKMGMTBEELAP	208			
Dd	: : : : : :	:	:	:	:
OY	289 EYEFOISSKPHLOKGKRWDSWSLRTQTPPEKPP	321			

RESULT 14	
08C7G1	
ID	08C7G1
AC	08C7G1
DT	01-MAR-2003 (TREMBlrel. 23, Created)
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE	Prolactin receptor related sequence 1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_Taxid=10090;
RM	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Liver;
RX	MEDLINE=22354683; PubMed=12466851;
RA	The FANTOM Consortium,
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RL	60,770 full-length cDNAs."
RL	Nature 420:565-573(2002).
SO	EMBL; AK050317; BAC34185.1; -. SEQUENCE 292 AA; 33618 MW; 9D60422B59E88A19 CRC64;

Query Match	17.3%	Score 194	DB 11	Length 292
Best Local Similarity	28.3%	Pred. No. 2.5e-10		
Matches 58; Conservative	37	Mismatches 92	Indels 18	Gaps 10

Dy 60 ASCSFFLPRIITPDNYTTEVEAENADGYIKSMYTWRLLENIAKTDPPK-IFRVAPVUGI 117

Dc 23 FGPKEPIHKCRSPDEKFTFCMMWPGSGGLPTVYSL--FYSKEGEKNATYECDPKYKSGPN- 79

Dy 3 TAKPENISGVYYRRKQLCTWSFGKETSY-IQYTAKRYTA-FGEHND-NCTTNSSISTNR 59

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Db      80  -SCFFSKQYTSIMKIYIIIVNATINEMSGSDPLVDVDTYIVEEBPPRNLTLEKQGVDK 138
Qy      118  KRMIOIETIKPELAPSS---DLKTLFFRVNSTSMMEVNFAPKRRDKQYVNLGTLP 174
Db      139  KYTLWKYKMLPPIITDVKTCMTFMEIYELIKSEBADEN-EIHFTHQIQ-----FRVPLYP 193
Qy      175  FTEYVIALFCANVSKSEKFSWDSQEK 199
Db      194  GKRYLVQTRCK--PDHGYSRWGQEK 217

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Q99JZ1	RESULT 15
ID	Q99JZ1
AC	Q99JZ1;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Prolactin receptor.
GN	PRLR.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Stauberg R.;
RL	Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC005555; AA00555.1; -
DR	EMBL; BC006652; AA006652.1; -
DR	HSSP; P16471; 1BP3.
DR	MGD; MGI:97763; P1r.
DR	InterPro; IPR002996; CRIA.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR003528; Hemtopoptn_L_F1.
DR	Pfam; PF00041; fn3; 2.
DR	SMART; SM00060; fn3; 2.
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW	Receptor.
Q0	SEQUENCE 608 AA; 68223 MW; 2710DAEC2B1A8F63 CRC64;

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Query March 17.0%; Score 191; DB 11; Length 608;
Best Local Similarity 27.8%; Pred. No. 1,2e-09;
Matches 57; Conservative 38; Mismatches 92; Indels 18; Gaps 10

QY 3 PAREPISCVYYRRKRLTCTMSPGKSTSY-TQYVYKRYLA-FGKH-D-NCTTSSITSENR 59
Db 23 PGPBPFLHKKRSPDKLFTCTMWPNGSDGLPTNYISL--TYSKEGKKNYEECPDYKTSGN- 79
QY 60 ASCSPFLPRITIPDVTYTEVEALENGDGYIKSMHTYWRLENIATKEPPK--IFRVKPLGI 117
Db 80 -SCFFSKQYTSIMKIYIITVANTNMGSSDPLVDVTYIVBEPPRNLTLEVKQKDK 138
QY 118 KRMIOLEWIKPELAYVSS---DKTTLRFRTVNSTSMNEVNFANRKRDKQTNLTGLQIP 174
Db 139 KYLAWKMLPPIITVYKGMFTMEYIKLKSBEADW-EIIFTHGQIQ-----FKVPDLYP 193
QY 175 FTEVYIALCAVAKESKFSMDMSQEK 199
Db 194 GQKYLQVTRCK-PDHGYSRMGQEK 217

Search completed: August 18, 2003, 13:30:16
Job time : 76.6152 secs

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Search completed: August 18, 2003, 13:30:16
Job time : 76.6152 secs

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CM protein - protein search, using sw model

Run on: August 18, 2003, 13:12:37 ; Search time 71.829 Seconds
(without alignments)
417.649 Million cell updates/sec

Title: US-09-892-949-2_COPY_544_732

Perfect score: 1017
Sequence: 1 KKPRLTTLCPWTPVNPAS.....VTAREFLVSEKLPHITKGEV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	100.0	620	22	ABG05070
2	1017	100.0	732	23	ABH050730
3	1017	100.0	764	24	ABP54365
4	1017	100.0	764	24	ABP54365
5	1010	99.3	745	23	AAE24024
6	514.5	50.6	649	23	ABH050738
7	514.5	50.6	662	22	AAH51244
8	514.5	50.6	662	23	AAE24029
9	514.5	50.6	662	23	ABH050741

10	514.5	50.6	681	24	ABP54363	Human NR10.3 splic
11	505	49.7	94	24	ABP54372	Human NR10.4 exon
12	483.5	47.5	716	24	ABP54370	Mouse NR10.4b-c
13	483.5	47.5	726	23	AAE24037	Mouse haematopoiet
14	479.5	47.1	716	24	ABP54371	Mouse NR10.5/BL-6
15	462	45.4	652	22	AAH51242	Human haematopoiet
16	462	45.4	652	23	AAE24028	Human HPR1 variant
17	304	29.9	662	23	ABH05742	Mouse zcytor17 pro
18	183	18.0	627	24	ABP54366	Human NR10.5 splic
19	96.5	9.5	851	19	AAW43079	HIV-1 gp120 protei
20	95.5	9.4	854	23	ABH06214	HIV Env isolate TV
21	95.5	9.4	854	24	ABH06568	Human immunodefici
22	95	9.3	513	20	AAW97587	Human immunodefici
23	95	9.3	849	21	AAH69346	HIV-1 non-subtype
24	92	9.0	491	19	AAW37057	HIV-1 breakthrough
25	92	9.0	858	23	AAH48951	HIV-1 subtype C is
26	92	9.0	1294	23	ABH78296	Amino acid sequenc
27	92	9.0	1349	19	AAW59359	Human retinal dege
28	91.5	9.0	619	23	AAU75156	N-terminal mutant
29	91.5	9.0	646	23	AAU75155	Modified full-leng
30	90.5	8.9	853	9	AAH81858	Sequence encoded b
31	90	8.8	486	19	AAW37056	HIV-1 breakthrough
32	90	8.8	846	21	AAH69353	HIV-1 non-subtype
33	89.5	8.8	853	22	AAH82762	Ancestral HIV-1 gr
34	89	8.8	883	22	AAH82761	Drosophila melanog
35	89	8.8	1846	22	AAH63163	HIV-1 gp120 protei
36	88	8.7	854	19	AAW43076	Human polypeptide
37	87.5	8.6	449	23	ABP69364	Herbicidally activ
38	87	8.6	615	23	ABH91483	HIV env protein fr
39	87	8.6	848	23	AAU11872	HIV-1 non-subtype
40	87	8.6	865	21	AAH69354	HIV-1 gp120 protei
41	86	8.5	503	22	AAH83355	Clone 25-1 encoded
42	86	8.5	801	12	AAH11742	Sequence deduced f
43	85	8.4	846	11	AAH08406	Human Ship-2 prote
44	85.5	8.4	1258	21	AAH80120	Human type 2 SH-2
45	85.5	8.4	1258	22	AAH98987	

ALIGNMENTS

RESULT 1
ABG05070 standard; Protein; 620 AA.

AC ABG05070;
13-FEB-2002 (first entry)

DE Novel human diagnostic protein #5061.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX WO200175067-A2.
XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI, 2001-639362/73.
XX N-PSDB; AAS69257.

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 35429; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging or sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations in
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 620 AA;
SO
Query Match 100.0%; Score 1017; DB 22; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKPNKLTLCMPVTPNPASSIATWGGDFDKDLNKSSDVSNTEDRLIKCSTPSDYL 60
DB 432 KKPNKLTLCMPVTPNPASSIATWGGDFDKDLNKSSDVSNTEDRLIKCSTPSDYL 491
QY VIDKLIVNFGNVLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELPVSPFI 120
DB 492 VIDKLIVNFGNVLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELPVSPFI 551
QY 121 PPKSQYLRSRMPEGTREPAKEQLLFSQSLVPHDLCEGAPNPYLKNSVTAREFLVSEK 180
DB 552 PPKSQYLRSRMPEGTREPAKEQLLFSQSLVPHDLCEGAPNPYLKNSVTAREFLVSEK 611
QY 181 LPEHTKGEV 189
DB 612 LPEHTKGEV 620
RESULT 2
ABG05730
ID ABG05730 standard; Protein; 732 AA.
XX
AC ABB05730;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human zcytor17 protein sequence SEQ ID NO:2.
XX
XX zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antiinflammatory; antiviral; antitubercular; antitubercular; cytostatic;
KW muscular; lymphoid; immune; inflammatory; spleenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreaticitis; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
PN WO200200721-A2.
XX
PD 03-JAN-2002.

XX
XX 26-JUN-2001; 2001WO-US20484.
PF
XX
XX 26-JUN-2000; 2000US-214282P.
PR
XX 29-JUN-2000; 2000US-214955P.
PR
XX 08-FEB-2001; 2001US-267963P.
XX
XX (ZYMO) ZYMOGENETICS INC.
PI
PI Sprecher CA, Preenell SR, Gao Z, Whitmore TE, Kujper JL;
PI Maurer MF;
XX
XX WPI; 2002-090519/12.
DR
XX N-PSDB; ABA93767.
XX
PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT spleenic, blood or bone disorders -
XX
XX Claim 18; Page 166-168; 235pp; English.
XX
XX The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
CC antitubercular, antitubercular and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, spleenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 732 AA;
SO
Query Match 100.0%; Score 1017; DB 23; Length 732;
Best Local Similarity 100.0%; Pred. No. 1.5e-93;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKPNKLTLCMPVTPNPASSIATWGGDFDKDLNKSSDVSNTEDRLIKCSTPSDYL 60
DB 544 KKPNKLTLCMPVTPNPASSIATWGGDFDKDLNKSSDVSNTEDRLIKCSTPSDYL 603
QY 61 VIDKLIVNFGNVLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELPVSPFI 120
DB 604 VIDKLIVNFGNVLQEIFTDEARTGQNNLGGKNGVYTCPPRPDCPLGKSFELPVSPFI 663
QY 121 PPKSQYLRSRMPEGTREPAKEQLLFSQSLVPHDLCEGAPNPYLKNSVTAREFLVSEK 180
DB 664 PPKSQYLRSRMPEGTREPAKEQLLFSQSLVPHDLCEGAPNPYLKNSVTAREFLVSEK 723
QY 181 LPEHTKGEV 189
DB 724 LPEHTKGEV 732
RESULT 3
ABP54364
ID ABP54364 standard; Protein; 764 AA.
XX
AC ABP54364;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.4 splicing variant protein SEQ ID NO:4.
XX
XX NR10; splicing variant; haematopoietic receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;

XX	km	haematopoietic disease; haematopoietic cell regulation.
XX	OS	Homo sapiens.
XX	PN	WO200277230-A1.
XX	PD	03-OCT-2002.
XX	PE	22-MAR-2002; 2002MO-JP02769.
XX	PR	26-MAR-2001; 2001JP-0087298.
XX	PA	(CHUS) CHUGAI SEIYAKU KK.
XX	PI	Maeda M, Yaguchi N, Hasegawa M;
XX	DR	WPI; 2003-018925/01.
XX	NF	N-PDSB; ABQ83364.
XX	PT	NR10 splicing variants of hematopoietin receptor proteins and encoded genes, applicable in searching hematopoietic factors and developing remedies for immunological and hematopoietic diseases -
XX	PS	Claim 1; Fig 6; 250pp; Japanese.
CC	CC	The present invention describes haematopoietic receptor NR10 splicing variants (I). (II) have immunomodulator and haemostatic activities. The proteins and encoded genes are applicable in searching for novel haematopoietic factors, and developing remedies for immunological and haematopoietic diseases. The haematopoietin receptor gene participate in vivo immunomodulation and haematopoietic cell regulation, and in the search for haematopoietic factors capable of functionally binding to the receptors. The present sequence represents the human NR10.4 protein from the present invention.
SQ	Sequence	764 AA;
Query Match	100.0%; Score 1017; DB 24; Length 764;	
Best Local Similarity	100.0%; Pred. No. 1.6e-93;	
Matches 189; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
Oy	1 KKPNTGLTLCWTVTPNPASSIAITHGDDFKKLNKESDSDVNTEDRLIKPCSTPSDKL 60	
Db	576 KKPNTGLTHCWTVTPNPASSIAITHGDDFKKLNKESDSDVNTEDRLIKCSTPSDKL 635	
Oy	VIDKLWNFGNVLQEIFTDERTGGENNIGERKNGVYVTRPPDCPLGKSFEELPVSPRI 120	
Db	636 VIDKLWNFGNVLQEIFTDERTGGNNNGEENGVYVTRPPDCPLGKSFEELPVSPRI 695	
Oy	121 PPKRSQVLRSRMPEESTRPEAKEQLLFSGSLVPDHLCEGAGNPYLKNSVTAREFLVSEK 180	
Db	696 PPKRSQVLRSRMPEESTRPEAKEQLLFSGSLVPDHLCEGAGNPYLKNSVTAREFLVSEK 755	
Oy	181 LPEHTKGEV 189	
Db	756 LPEHTKGEV 764	
RESULT 4		
ABP54365		
ID	ABP54365 standard; Protein; 764 AA.	
AC	ABP54365;	
XX		
DT	20-JAN-2003 (first entry)	
XX		
DE	Human NR10.4 splicing variant protein SEQ ID NO:6.	
XX		
KW	NR10; splicing variant; haematopoietin receptor; immunomodulator;	
KW	haemostatic; haematopoietic factor; immunological disease;	
KW	haematopoietic disease; haematopoietic cell regulation.	
XX		
OS	Homo sapiens	

XX	WO200277230-A1.
PN	
XX	03-OCT-2002.
PD	
XX	22-MAR-2002; 2002WO-JP02769.
PF	
XX	26-MAR-2001; 2001JP-0087298.
PR	
XX	(CHUS) CHUGAI SEIYAKU KK.
PA	
XX	Maeda M, Yaguchi N, Hasegawa M;
PL	
XX	WPI; 2003-018925/01.
DR	
XX	N-PSDB; ABQ93365.
PT	
XX	NR10 splicing variants of hematopoietin receptor proteins and encoded
PT	genes, applicable in searching hematopoietic factors and developing
FT	remedies for immunological and hematopoietic diseases -
XX	
PS	
XX	Claim 1; Fig 7-9; 250pp; Japanese.
XX	
CC	The present invention describes hematopoietic receptor NR10 splicing
CC	variants (I). (I) have immunomodulator and haemostatic activities. The
CC	proteins and encoded genes are applicable in searching for novel
CC	haematopoietic factors, and developing remedies for immunological and
CC	haematopoietic diseases. The haematopoietin receptor genes participate
CC	in in vivo immunomodulation and hematopoietic cell regulation, and in
CC	the search for haematopoietic factors capable of functionally binding
CC	to the receptors. The present sequence represents the human NR10.4
CC	protein from the present invention.
XX	
XX	Sequence 764 AA;

Query Match	100.0%	Score 1017	DB 24	Length 764
Best Local Similarity	100.0%	Pred. No. 1.6e-93		
Matches 189	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	KKPNKLTHLCMPYVNPNAESSIATWGHGDFKDKLNLKESGDSVNTEDRIKCPSTPSDKL	60	
Db	576	KKPKMLTHLCMPYVNPNAESSIATWGHGDFKDKLNLKESGDSVNTEDRIKCPSTPSDKL	6355	
QY	61	VIDKLNVNFGVNLQEIFTDEARTGOENNLGGEKNGVYTCPPRPDCPLGKSFEELPVSPET	1200	
Db	636	VIDKLNVNFGVNLQEIFTDEARTGOENNLGGEKNGVYTCPPRPDCPLGKSFEELPVSPET	6955	
QY	121	PPRSQYVRSRMPSTREPAKEQLLFSGQSLVPDHLCEBGANPYLKNSTVAREFLVSEK	180	
Db	696	PPRSQYVRSRMPSTREPAKEQLLFSGQSLVPDHLCEBGANPYLKNSTVAREFLVSEK	755	
QY	181	LPHTKGEV	189	
Db	756	LPHTKGEV	764	
RESULT 5				
AAE24024	ID	AAE24024 standard; Protein; 745 AA.		
XX	AAE24024;			
AC				
XX				
DT	23-SEP-2002 (first entry)			
XX				
DE	Human haematopoietin receptor 1 (HPR1) protein.			
XX				
KM	Human; haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;			
KM	pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;			
KM	neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;			
KM	cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;			
KM	ITP; sickle cell vasoocclusive crisis; myelofibrosis; myeloid metaplasia;			
KM	osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;			
KM	anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;			
KM	demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;			

KM vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
KM stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
XX ischaemic disease.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 20..32 /label= Signal_peptide
FT Protein 33..745 /note= "Human mature HPRI protein"
FT Domain 33..241 /note= "Cytokine receptor domain"
FT Misc-difference 83 /note= "This residue changes to Ala during
allelic variation"
FT Domain 135..138 /note= "Proline-rich linker"
FT Domain 139..241 /note= "C-terminal cytokine receptor subdomain"
FT Misc-difference 168 /note= "This residue changes to Asn during
allelic variation"
FT Misc-difference 187 /note= "This residue changes to Thr during
allelic variation"
FT Misc-difference 224..228 /note= "MSXMS motif"
FT Region 242..515 /note= "Fibronectin repeat"
FT Misc-difference 361 /note= "This residue changes to Pro during
allelic variation"
FT Misc-difference 362 /note= "This residue changes to Gly during
allelic variation"
FT Misc-difference 510 /note= "This residue changes to Asn during
allelic variation"
FT Misc-difference 517 /note= "Encoded by GAC. This residue changes to
Asp during allelic variation"
FT Domain 526..556 /note= "Extended transmembrane domain"
FT Domain 533..552 /note= "Core transmembrane domain"
FT Domain 553..745 /note= "Cytoplasmic domain"
FT Domain 563..573 /note= "Box1 conserved motif"
FT Region 588..592 /note= "Repeat peptide"
FT Region 597..601 /note= "Repeat peptide"
FT Region 603..607 /note= "Repeat peptide"
FT Region 614..618 /note= "Repeat peptide"
FT Region 619..623 /note= "Repeat peptide"
FT Domain 631..641 /note= "Repeat peptide"
FT Domain /note= "Box2 conserved motif"
FT Region 635..639 /note= "Repeat peptide"
FT Misc-difference 679 /note= "This residue changes to Gly during
allelic variation"

XX 06-OCT-2000; 2000US-238706P.
PR 13-OCT-2000; 2000US-240476P.
PR 20-FEB-2001; 2001US-270282P.
XX
XX (IMMUNEX CORP.
XX
XX Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,
PI WPI, 2002-330172/36.
DR N-PSDB; AAD38772.
XX
XX Human and murine hematopoietin receptor polypeptides HPRI and HPR2,
PT useful for treating cell proliferation, metabolic, and reproductive
PT hormone related conditions -
XX
XX Claim 1; Page 84-87; 136pp; English.

PS The present invention relates to human and murine haematopoietin receptor
XX polypeptides HPRI and HPR2. Sequences of the invention are useful for
CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
CC resulting from a lack of bone-forming cells. They are also useful for
CC treating cell proliferation conditions such as leukaemia and tumour
CC metastasis, osteoporosis resulting from an excess of bone-resorbing
CC cells. HPR sequences are also useful for treating medical conditions and
CC diseases such as cell proliferation, metabolic and reproductive hormone
CC related conditions. They are useful for treating various haematologic and
CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
CC dysplastic syndromes (including refractory anaemia, refractory anaemia
CC with ringed sideroblasts or with excess blasts), idiopathic thrombocy-
CC paenic purpura (ITP), sickle cell vasoocclusive crisis, myelofibrosis/
CC myeloid metaplasia, osteoclast disorders that lead to bone loss such
CC as osteoporosis including post-menopausal osteoporosis, periodontitis
CC resulting in tooth loosening or loss, prosthesis loosening after joint
CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
CC myasthenia gravis, chronic neuronal degeneration, stroke including
CC cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful
CC for treating various other disorders such as osteoporosis, obesity,
CC deficient mammary development and infertility. The present sequence
CC is human HPRI protein.
XX
XX

SO Sequence 745 AA;

Query Match 99.3%; Score 1010; DB 23; Length 745;
Best Local Similarity 99.5%; Pred. No. 7; 8e-93;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKNPLTLHCWPTVNPAPASSIATWHDGDFKDKLTKSSDSVNTEDRTLRKCSPPSDTL 60
DB 557 KKNPLTLHCWPTVNPAPASSIATWHDGDFKDKLTKSSDSVNTEDRTLRKCSPPSDTL 616
QY 61 VIDKLIVNFGNVLQEIFTDGARTQENNLGSKNGVYTCPPRPDCLGSPFELVSPRI 120
DB 617 VIDKLIVNFGNVLQEIFTDGARTQENNLGSKNGVYTCPPRPDCLGSPFELVSPRI 676
QY 121 PPKSQYLRSNMPGCTRPAPKQQLFSGQSLVPDHLCEGADNPYLKNSVTAREPLVSEK 180
DB 677 PPKSQYLRSNMPGCTRPAPKQQLFSGQSLVPDHLCEGADNPYLKNSVTAREPLVSEK 736
QY 181 LPEHTKGEV 189
DB 737 LPEHTKGEV 745

XX	AB05738	standard; Protein; 649 AA.
ID	AB05738	
XX	AB05738;	
XX	01-MAY-2002	(first entry)
XX	Human zcytor17 protein sequence SRQ ID NO:46.	
XX		
XX	Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;	
XX	antifibrotic; antiviral; antithrombotic; antidiabetic; cytoprotective;	
XX	muscular; lymphoid; immune; inflammatory; splenic; bone;	
XX	infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;	
XX	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;	
XX	inflammatory disease; pancreatitis; inflammatory bowel disease.	
XX		
XX	Homo sapiens.	
XX		
XX	MO20020721-A2.	
XX		
XX	03-JAN-2002.	
XX		
XX	26-JUN-2001; 2001MO-US20484.	
XX		
XX	26-JUN-2000; 2000US-214282P.	
XX	29-JUN-2000; 2000US-214955P.	
XX	08-FEB-2001; 2001US-267963P.	
XX		
XX	(ZYMO) ZYMOGENETICS INC.	
XX		
XX	Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JJ,	
XX	Maurer MF;	
XX		
XX	WPI; 2002-090519/12.	
XX	N-PSDB; ABA93803.	
XX		
XX	Isolated polynucleotide encoding a cytokine receptor zcytor17 which is	
XX	useful for treating and diagnosing lymphoid, immune, inflammatory,	
XX	splenic, blood or bone disorders -	
XX		
XX	Claim 18; Page 195-197; 235P; English.	
XX		
XX	The present invention describes a cytokine receptor designated zcytor17.	
XX	Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,	
XX	antirheumatic, antidiabetic and muscular activities. The zcytor17	
XX	proteins are useful for treating and diagnosing lymphoid, immune,	
XX	inflammatory, splenic, blood or bone disorders. Agonists or	
XX	anti-zcytor17 antibodies are useful in stimulating cell-mediated	
XX	immunity and for stimulating lymphocyte proliferation, such as in the	
XX	treatment of infections involving immunosuppression, including certain	
XX	viral infections. They are also useful for inducing cytotoxicity and	
XX	for treating leukopenia. Antagonist of zcytor17 polypeptides are useful	
XX	for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple	
XX	sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,	
XX	pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to	
XX	chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to	
XX	ABA93843 and ABB05730 to ABB05745 represent sequences used in the	
XX	exemplification of the present invention.	
XX		
XX	Sequence 649 AA;	
XX		
XX	Query Match 50.6%; Score 514.5; DB 23; Length 649;	
XX	Best Local Similarity 94.2%; Pred. No. 6,1e-43;	
XX	Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;	
XX		
XX	1 KKNKLTLLCHPTVNPAPASSIATAGHGFQDKNLKSSDVSVNEDRIILKPCSTPSDKL 60	
XX	544 KKNKLTLLCHPTVNPAPASSIATAGHGFQDKNLKSSDVSVNEDRIILKPCSTPSDKL 603	
XX	61 VIDKLVPFNVGLQEIFTDGARTGNNLGGKNG--VYTCP 100	

```

Db      604 VIDKLNVNFGVNLQEIFTDDEARTGQENNLGGEEKNGTRILSSCP 646

RESULT 7
ID      AAB51244 standard; Protein; 662 AA.
XX      AAB51244;
AC      AAB51244;
DT      26-MAR-2001 (first entry)
DE      Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.
XX      Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW      immunoregulation; haematopoietic cell regulation; transmembrane;
KW      immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KM      metal allergy; pollen allergy.
XX      Homo sapiens.
OS      WO200075314-A1.
PD      14-DEC-2000.
PE      01-JUN-2000; 2000WO-JP03556.
PR      02-JUN-1999; 99JP-0155797.
PS      30-JUL-1999; 99JP-0217979.
XX      (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA      Maeda M, Yaguchi N;
PI      WPI: 2001-061720/07.
DR      N-PSDB; AAC92350.
PT      Hematopoietin receptor protein NR10 for screening potential ligands for
PT      treatment of immune and hematopoietic disorders such as autoimmune
PT      diseases and allergies -
XX      Claim 1; Fig 13-14; 127dp; Japanese.
PS      The present sequence represents a human haemopoietin receptor protein
CC      (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
CC      protein and a soluble protein. NR10.3. NR10 occurs as a transmembrane
CC      protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC      which participates in immunoregulation and haematopoietic cell
CC      regulation in vivo, and is useful in searching for haematopoietic
CC      factors capable of binding to the receptor. NR10 can be used for the
CC      identification of substances for the treatment and prevention of immune
CC      and haematopoietic disorders including autoimmune diseases and allergies
CC      such as metal and pollen allergy.
SQ      Sequence 662 AA;

Query Match          50.6%; Score 514.5; DB:22; Length 662;
Best Local Similarity 94.2%; Pred.No.6.2e+43;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1

Oy      1 KKPKNKLTHTLCMPVPNPDAESSIATWGHDDFKDKLNTLKESDSDSVATEDRILKPCSTPSDXL 60
Db      557 KKPKPLTHTLCMPYTPNPDAESSIATWGHDDFDKDLNKESDSDSVATEDRILKPCSTPSDXL 616
Oy      61 VIDKLNVNFGVNLQEIFTDDEARTGQENNLGGEEKNG---YTCGP 100
Db      617 VIDKLNVNFGVNLQEIFTDDEARTGQENNLGGEEKNGTRILSSCP 659

RESULT 8
ID      AAE24029 standard; Protein; 662 AA.
XX      AAE24029;
AC      AAE24029;
DT      26-MAR-2001 (first entry)
DE      Human haemopoietin receptor protein NR10.3 SEQ ID NO:17.
XX      Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW      immunoregulation; haematopoietic cell regulation; transmembrane;
KW      immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KM      metal allergy; pollen allergy.
XX      Homo sapiens.
OS      WO200075314-A1.
PD      14-DEC-2000.
PE      01-JUN-2000; 2000WO-JP03556.
PR      02-JUN-1999; 99JP-0155797.
PS      30-JUL-1999; 99JP-0217979.
XX      (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
PA      Maeda M, Yaguchi N;
PI      WPI: 2001-061720/07.
DR      N-PSDB; AAC92350.
PT      Hematopoietin receptor protein NR10 for screening potential ligands for
PT      treatment of immune and hematopoietic disorders such as autoimmune
PT      diseases and allergies -
XX      Claim 1; Fig 13-14; 127dp; Japanese.
PS      The present sequence represents a human haemopoietin receptor protein
CC      (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
CC      protein and a soluble protein. NR10.3. NR10 occurs as a transmembrane
CC      protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC      which participates in immunoregulation and haematopoietic cell
CC      regulation in vivo, and is useful in searching for haematopoietic
CC      factors capable of binding to the receptor. NR10 can be used for the
CC      identification of substances for the treatment and prevention of immune
CC      and haematopoietic disorders including autoimmune diseases and allergies
CC      such as metal and pollen allergy.
SQ      Sequence 662 AA;

Query Match          50.6%; Score 514.5; DB:22; Length 662;
Best Local Similarity 94.2%; Pred.No.6.2e+43;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1

Oy      1 KKPKNKLTHTLCMPVPNPDAESSIATWGHDDFKDKLNTLKESDSDSVATEDRILKPCSTPSDXL 60
Db      557 KKPKPLTHTLCMPYTPNPDAESSIATWGHDDFDKDLNKESDSDSVATEDRILKPCSTPSDXL 616
Oy      61 VIDKLNVNFGVNLQEIFTDDEARTGQENNLGGEEKNG---YTCGP 100
Db      617 VIDKLNVNFGVNLQEIFTDDEARTGQENNLGGEEKNGTRILSSCP 659

```

DT 23-SEP-2002 (first entry)
 XX Human HPRI variant protein #3.
 XX
 XX Human: haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;
 KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
 KW neurodegenerative disorder; leukaemia; carcinoma; haematologic purpura;
 KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KW osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;
 KW anorexia nervosa; chronic fatigue syndrome; Crenzfeld-Jacob disease;
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 KW stroke; fatigue; tumor; sarcoma; osteoporosis; obesity; infertility;
 KW ischaemic disease; variant.
 XX
 XX Homo sapiens.
 XX
 XX MO200229060-A2.
 XX
 XX 11-APR-2002.
 XX
 XX 05-OCT-2001; 2001MO-US31634.
 XX
 XX 06-OCT-2000; 2000US-238706P.
 XX 13-OCT-2000; 2000US-240476P.
 XX 20-FEB-2001; 2001US-270282P.
 XX
 XX (IMMW) IMMUNEX CORP.
 XX
 XX Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
 XX WPI; 2002-330172/36.
 XX
 XX Human and murine hemapoietin receptor polypeptides HPRI and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions -
 PT
 XX Disclosure; Page 112-115; 136pp; English.
 XX
 XX The present invention relates to human and murine haematopoietin receptor
 CC polypeptides HPRI and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukaemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various haematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polynuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeld-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC myasthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence
 CC is human HPRI variant protein.

SQL Sequence 662 AA;
 Query Match 50.6%; Score 514.5; DB 23; Length 662;
 Best Local Similarity 94.2%; Pred. No. 6.2e-43;
 Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;
 QY 1 KKPNTLTLCPVTENPAPSSIAIWHGDFDKDNLKESDSDVNTEDRIKCPSPDKL 60
 DB 557 KKPNTLTLCPVTENPAPSSIAIWHGDFDKDNLKESDSDVNTEDRIKCPSPDKL 616
 QY 61 VLDKLVNPGNVLQGEIPTDEARTGQNNLGGKNG---YVTP 100
 DB 617 VLDKLVNPGNVLQGEIPTDEARTGQNNLGGKNGKTRILLSCP 659
 RESULT 9
 ABB05741
 ID ABB05741 standard; Protein; 662 AA.
 AC ABB05741;
 XX
 XX 01-MAY-2002 (first entry)
 DT
 XX
 XX Human zcytor17 protein sequence SEQ ID NO:54.
 DE
 XX zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 KW antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW inflammatory disease; pancreatitis; inflammatory bowel disease.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200200721-A2.
 PN
 XX 03-JAN-2002.
 PD
 XX
 XX 26-JUN-2001; 2001MO-US20484.
 PF
 XX
 XX 26-JUN-2000; 2000US-214282P.
 PR 29-JUN-2000; 2000US-214955P.
 PR 08-FEB-2001; 2001US-267963P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kujiiper JL;
 PI Maurer MF;
 PI WPI; 2002-090519/12.
 DR N-PSDB; ABA93808.
 XX
 XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 PT useful for treating and diagnosing lymphoid, immune, inflammatory,
 PT splenic, blood or bone disorders -
 PT
 XX Example 1; Page 204-206; 235pp; English.
 XX
 XX The present invention describes a cytokine receptor designated zcytor17.
 CC zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiarthritic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, including in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreaticitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the

CC exemplification of the present invention.

XX Sequence 662 AA;

Query Match 50.6%; Score 514.5; DB 23; Length 662;
Best Local Similarity 94.2%; Pred. No. 6.2e-43;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPENKLTLCWPTVPNPASSIATWGGDFKDKLANKESDSDSVNTEDRILKPCSTPSDKL 60
DB 557 KKPENKLTLCWPTVPNPASSIATWGGDFKDKLANKESDSDSVNTEDRILKPCSTPSDKL 616

QY 61 VIDKLNVNFGNVLQEIFTDARTGQNNLIGERKNG---YVTCF 100
DB 617 VIDKLNVNFGNVLQEIFTDARTGQNNLIGERKNGTRILSSCP 659

RESULT 10
ID ABP54363 standard; Protein; 681 AA.

AC ABP54363;
XX 20-JAN-2003 (first entry)

DE Human NR10.3 splicing variant protein SEQ ID NO:2.

KW NR10, splicing variant; haematopoietic receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

PN MO200277230-A1.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

XX WPI: 2003-018925/01.

DR N-PSDB; AB083363.

XX NR10 splicing variants of hematopoietic receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -

XX Example 2; Fig 3; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietic receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.3
CC protein from the present invention.

XX Sequence 681 AA;

Query Match 50.6%; Score 514.5; DB 24; Length 681;
Best Local Similarity 94.2%; Pred. No. 6.5e-43;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPENKLTLCWPTVPNPASSIATWGGDFKDKLANKESDSDSVNTEDRILKPCSTPSDKL 60
DB 576 KKPENKLTLCWPTVPNPASSIATWGGDFKDKLANKESDSDSVNTEDRILKPCSTPSDKL 635

QY 61 VIDKLNVNFGNVLQEIFTDARTGQNNLIGERKNG---YVTCF 100
DB 636 VIDKLNVNFGNVLQEIFTDARTGQNNLIGERKNGTRILSSCP 678

RESULT 11
ID ABP54372 standard; Protein; 94 AA.

AC ABP54372;

XX 20-JAN-2003 (first entry)

DE Human NR10.4 exon CP10-4 amino acid sequence SEQ ID NO:21.

KW NR10, splicing variant; haematopoietic receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation.

OS Homo sapiens.

PN MO200277230-A1.

PD 03-OCT-2002.

PF 22-MAR-2002; 2002WO-JP02769.

PR 26-MAR-2001; 2001JP-0087298.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Maeda M, Yaguchi N, Hasegawa M;

XX WPI: 2003-018925/01.

DR N-PSDB; AB083373.

XX NR10 splicing variants of hematopoietic receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -
XX disclosure; Page 238-239; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietic receptor genes participate
CC in vivo immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.4 exon
CC CP10.4 amino acid sequence from the present invention.

XX Sequence 94 AA;

Query Match 49.7%; Score 505; DB 24; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.2e-43;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 YVTCFPRPDCPIGKSFELPVSPPEIPRKSQYLRSMPEGTPEAKQQLFSGQSLVDPH 155
DB 1 YVTCFPRPDCPIGKSFELPVSPPEIPRKSQYLRSMPEGTPEAKQQLFSGQSLVDPH 60

QY 156 LCEBGAHPNYLKNSTYARFVSEKLPENTKGEV 189
DB 61 LCEBGAHPNYLKNSTYARFVSEKLPENTKGEV 94

RESULT 12
ID ABP54370 standard; Protein; 716 AA.

XX ABP54370;

The present invention relates to human and murine haematopoietic receptor polypeptides HPR1 and HPR2. Sequences of the invention are useful for treating cell proliferation conditions e.g., pancytopenia, leukopenia, anaemia, thrombocytopaenia, neurodegenerative disorders and osteoporosis resulting from a lack of bone-forming cells. They are also useful for treating cell proliferation conditions such as leukaemia and tumour metastasis, osteoporosis resulting from an excess of bone-resorbing cells. HPR sequences are also useful for treating medical conditions and diseases such as cell proliferation, metabolic and reproductive hormone related disorders. They are useful for treating various haematologic and oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell, cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma, sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer), squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia of chronic diseases, aplastic anaemia, Fanconi's aplastic anaemia), myelodysplastic syndromes (including refractory anaemia, refractory anaemia with ringed sideroblasts or with excess blasts), idiopathic thrombocytopenic purpura (ITP), sickle cell vasoocclusive crisis, myelofibrosis/myeloid metaplasia, osteoclast disorders that lead to bone loss such as osteoporosis including post-menopausal osteoporosis, periodontitis resulting in tooth loosening or loss, prosthesis loosening after joint replacement, neurodegenerative conditions (e.g., acute polymyopathy, Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy, Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome, myasthenia gravis, chronic neuronal degeneration, stroke including cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful for treating various other disorders such as osteoporosis, obesity, deficient mammary development and infertility. The present sequence is mouse HPR1 protein.

Query Match	Best Local Similarity	47.5%	Score 483.5	DB 23	Length 726
Matches 107	Conservative	20	Mismatches 57	Indels 7	Gaps 4
QY	1	KKPNKLTILCWPTVNPAPBASSIATWGHGDFKDKNLKSSDSSVNTEDRIILKPCSTPDKL	60		
DB	541	KKPNKLTILCPDVENPAPBASSIATWGHGDFKDKNLKSSDSSVNTEDRIILKPCSTPDKL	597		
QY	61	VLDKLVNFGNVLQGIIFTDARTGGNNLGGKNGYVTCFPPDCLKSPBELVASEI	120		
DB	558	LIDKLVNFGNVLQGIIFTDARTGGNNLGGKNGYVTCFPPDCLKSPBELVASEI	657		
QY	121	PPRKQYLRSMPEGTREPEAKQLLFSGOS--LVVDHLCESGAPNPKLVNSTVAREPLVS	178		
DB	658	ASDSDHSTCSRNADAEYSELARQPSSSCGSPQLSPR--EDQAQNPYLKNSVTTREPLVH	715		
QY	179	EKLPEHTKGEV	189		
DB	716	ENLPEHSGEV	726		

RESULT 14	
ABP54371	
ID	ABP54371 standard; Protein; 716 AA.
XX	
AC	ABP54371;
XX	
DT	20-JAN-2003 (first entry)
XX	
DE	Mouse mNR10c57BL-6 splicing variant protein SEQ ID NO:18.
XX	
KM	NR10; splicing variant; haematopoietin receptor; immunomodulator
KM	haemostatic; haematopoietic factor; immunological disease;
KM	haematopoietic disease; haematopoietic cell regulation.
XX	
OS	Mus musculus.
XX	
PN	WO200277230-A1.

PD	03-OCT-2002.
XX	
PF	22-MAR-2002; 2002WO-JP02769.
XX	
PR	26-MAR-2001; 2001JP-0087298.
XX	
PA	(CHUS) CHUGAI SEIYAKU KK.
XX	
PI	Maeda M, Yaguchi N, Hasegawa M;
XX	
DR	WPI; 2003-018925/01.
XX	
DR	N-PSDB; ABQ83371.
XX	
PT	NR10 splicing variants of hematopoietin receptor proteins and encoded
PT	genes, applicable in searching hematopoietic factors and developing
PT	remedies for immunological and hematopoietic diseases -
XX	
PS	Claim 1; Fig 33-35; 250pp; Japanese.
XX	
CC	The present invention describes haematopoietic receptor NR10 splicing
CC	variants (I). (I) have immunomodulator and haemostatic activities. The
CC	proteins and encoded genes are applicable in searching for novel
CC	haematopoietic factors, and developing remedies for immunological and
CC	haematopoietic diseases. The haematopoietin receptor genes participate
CC	in in vivo immunomodulation and haematopoietic cell regulation, and in
CC	the search for haematopoietic factors capable of functionally binding
CC	to the receptors. The present sequence represents the mouse mNR10c57BL-6
XX	protein from the present invention.

Query Match: Best Local Similarity Matches	716 AA, Conservative	47.1%; 56.0%;	Score 479.5; Pred. No. 2.3e-39;	DB 24;	Length 716;	Mismatches 57;	Indels 7;	Gaps 4
QY	1 KPNKLTLICPTVPNPASSIATWGHGDFKDKLTKSDSDSVNTEDRIKLCSTPSDKL	60						
Db	531 KPNRLTPLCCPDVNPASSIATWLGDPFK-KSNMKETGNSGDTEDVYLKFCVPAD--	587						
QY	61 VIDKLNVNFGVNLQEIFTDERTGQENNLGGEKKNVYTCPPRPDCPLGKSFEELPVSPET	120						
Db	588 LIDKLNVNFGVNLQEIFTDERTGQENNLGGEKKNVYTCPPRPDCPLGKSFEELPVSPET	647						
QY	121 PPRKSQYLRSMPECTREPEAKEQLLFSGQS--LVVDHLCSEGAPNPYLKNSVTAREFLVS	178						
Db	648 ASBDSHSTCSMADBEAYSLARQPSQSPSLSPR--EDQAQNPYLKNSVTAREFLVH	705						
QY	179 EKLPEHTKGEV	189						
Db	706 ENLPEHSGKEV	716						

RESULT 15	
AA851242	
ID	AA851242 standard; Protein; 652 AA.
XX	
AC	AA851242;
XX	
DT	26-MAR-2001 (first entry)
XX	
DE	Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.
XX	
KW	Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
KW	immunoregulation; haematopoietic cell regulation; transmembrane;
KW	immune disorder; haematopoietic disorder; autoimmune disease; allergy;
KW	metal allergy; pollen allergy.
XX	
OS	Homo sapiens.
XX	
PN	WO200075314-A1.
XX	
PD	14-DEC-2000.

```

XX 01-JUN-2000; 2000WO-JP03556.
PF
XX
PR 02-JUN-1999; 99JP-0155797.
PR 30-JUL-1999; 99JP-0217797.
XX
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Maeda M, Yaguchi N;
XX
DR WPI; 2001-061720/07.
DR N-PSDB; AAC92337.
XX
PT Hematopoietin receptor protein NR10 for screening potential ligands for
PT treatment of immune and hematopoietic disorders such as autoimmune
PT diseases and allergies -
XX
PS Claim 1; Fig 3-5; 127pp; Japanese.
XX
CC The present sequence represents a human haemopoietin receptor protein
CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
CC which participates in immunoregulation and haematopoietic cell
CC regulation in vivo, and is useful in searching for haematopoietic
CC factors capable of binding to the receptor. NR10 can be used for the
CC identification of substances for the treatment and prevention of immune
CC and haematopoietic disorders including autoimmune diseases and allergies
CC such as metal and pollen allergy.
XX
SQ Sequence 652 AA;

```

```

Query Match      45.4%; Score 462; DB 22; Length 652;
Best Local Similarity 100.0%; Pred. No. 1.2e-37;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKPKLTHLCWPTVPNPASSIATWGGDDPKDKLNLKESDSDSVNTEDRIILKPCSTPSDKL 60
   |||||||
DB 557 KKPKLTHLCWPTVPNPASSIATWGGDDPKDKLNLKESDSDSVNTEDRIILKPCSTPSDKL 616
   |||||||

QY 61 VIDKLIVNFGNVLOEFTDEARTGOE 86
   |||||||
DB 617 VIDKLIVNFGNVLOEFTDEARTGOE 642
   |||||||

```

Search completed: August 18, 2003, 13:27:01
 Job time : 72.829 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:24:23 ; Search time 23.3444 Seconds
(without alignments)
342.555 Million cell updates/sec

Title: US-09-892-949-2_COPY_544_732

Perfect score: 1017
Sequence: 1 KKPNTLTHLCWPTVPNPAS.....VTAREFLVSEKLPHETKGEV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	92	9.0	491	3	US-08-889-841B-10
2	92	9.0	491	4	US-09-419-362-10
3	92	9.0	1349	3	US-08-938-291A-6
4	92	9.0	1349	4	US-09-589-619-6
5	90.5	8.9	508	4	US-08-472-240A-16
6	90.5	8.9	853	4	US-09-206-551-13
7	90.5	8.9	872	3	US-07-556-483-12
8	90	8.8	486	3	US-08-889-841B-8
9	90	8.8	486	4	US-09-419-362-8
10	86.5	8.5	855	4	US-09-206-551-11
11	86.5	8.5	855	4	US-09-206-551-12
12	86	8.5	423	4	US-09-252-991A-26008
13	86	8.5	855	3	US-07-556-483-14
14	85	8.4	887	3	US-08-472-240A-5
15	84.5	8.3	495	3	US-08-889-841B-28
16	84.5	8.3	495	4	US-09-419-362-28
17	84	8.3	665	2	US-08-448-603A-32
18	84	8.3	665	4	US-08-448-603A-32
19	84	8.3	665	4	US-09-134-075-32
20	84	8.3	665	4	US-09-492-739-32
21	82	8.1	855	1	US-08-022-835-6
22	82	8.1	855	1	US-08-388-809-6
23	81.5	8.0	474	3	US-08-889-841B-36
24	81.5	8.0	474	3	US-08-889-841B-36
25	81.5	8.0	474	4	US-09-419-362-36
26	81.5	8.0	474	4	US-09-419-362-39
27	81	8.0	364	3	US-09-085-305-6

28	81	8.0	479	2	US-08-037-816A-20	Sequence 20, Appl
29	81	8.0	479	2	US-08-037-816A-24	Sequence 24, Appl
30	81	8.0	479	2	US-08-530-146-20	Sequence 20, Appl
31	81	8.0	479	2	US-08-530-146-24	Sequence 24, Appl
32	81	8.0	495	3	US-08-889-841B-25	Sequence 25, Appl
33	81	8.0	495	4	US-09-419-362-25	Sequence 25, Appl
34	81	8.0	507	4	US-08-037-816A-16	Sequence 16, Appl
35	81	8.0	507	2	US-08-037-816A-16	Sequence 16, Appl
36	81	8.0	507	2	US-08-037-816A-28	Sequence 28, Appl
37	81	8.0	507	2	US-08-530-146-16	Sequence 16, Appl
38	81	8.0	507	2	US-08-530-146-28	Sequence 28, Appl
39	80	7.9	484	2	US-08-037-816A-22	Sequence 22, Appl
40	80	7.9	484	2	US-08-530-146-22	Sequence 22, Appl
41	80	7.9	491	2	US-08-037-816A-18	Sequence 18, Appl
42	80	7.9	491	2	US-08-530-146-18	Sequence 18, Appl
43	80	7.9	516	4	US-08-817-441-48	Sequence 48, Appl
44	80	7.9	520	2	US-08-037-816A-14	Sequence 14, Appl
45	80	7.9	520	2	US-08-037-816A-26	Sequence 26, Appl

ALIGNMENTS

```
RESULT 1
US-08-889-841B-10
; Sequence 10, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Bertman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 491
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-10

Query Match
Best Local Similarity 23.0%; Score 92; DB 3; Length 491;
Matches 49; Conservative 23; Mismatches 69; Indels 72; Gaps 8;

QY 7 TLICMPYVNPRESSI--ATWHDGDFKDKLNKESDVSNTEDRLKPCSTPSDKLVYDK 64
DB 30 THACVPTDNPQEVVLENTENFNMMKNMVEQMHEDIISLMDQSLKCV---KLTPLC 85
QY 65 LVVNFQNVYQELFTDEARTGQENNIGGEKGVVTPRPRDCL---GK----- 109
DB 86 VTLNCTNLNANNNTNANNNTNNTYTLGEMERGEKNCSPNITTSLRDKKKEVLYFKLDV 145
QY 110 -----SFEELPVSPRIP-----PRKQY 127
DB 146 QINDSTNVRLLISCVTSVITQACPKVSPFPIPHYCAPAGFALCKDKKFNGTGCKN-- 203
QY 128 LRS-RMPEGTREPAKEQLFSGOSLVPDLCEE 159
DB 204 VRTVQCTHGRIRVSVSTOLLNGS-----LAEE 230

RESULT 2
US-09-419-362-10
; Sequence 10, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Bertman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIVI
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
```

;; PRIOR APPLICATION NUMBER: US 08/889,841
;; PRIOR FILING DATE: 1997-07-08
;; PRIOR APPLICATION NUMBER: US 60/676,737
;; PRIOR FILING DATE: 1996-07-08
;; NUMBER OF SEQ ID NOS: 57
;; SOFTWARE: PasteSeq for Windows Version 3.0
;; SEQ ID NO 10
;; LENGTH: 491
;; TYPE: PRT
;; ORGANISM: HIV
US-09-419-362-10

Query Match 9.0%; Score 92; DB 4; Length 491;
Best Local Similarity 23.0%; Pred. No. 0.12;
Matches 49; Conservative 23; Mismatches 69; Indels 72; Gaps 8;

QY 7 THLCWVPVPPASSI--ATWGGDDPKDKLNKESDVSUTEDRIILKPGSTPDKVIDK 64
DB 30 THACVFPDPQEVLENTVENFMNMKNVQMHEDITSLWDQSLKPCV---KLTPLC 85
QY 65 LVNFGVNLQEIFTEARTGOENNLGEGKNGVTCFPRDPCPL---GK----- 109
DB 86 VTLCNLTENANNTEANNNTNNTLGMERGERKNCSEFNITSLADKQKEVALFYLDVY 145
QY 110 -----SPEELVPSPEIP-----PKSQY 127
DB 146 QIDNSTVYRLISGTSVITQACPKVSFEPIPIHYCAPAGFALIKCKDKKNGTGPCKN-- 203
QY 128 LRS-RMPEGRPEAKQOLLESGQSLVPDHCCE 159
DB 204 VRTVQCTHGIRPVSTQLNLNGS-----LAEE 230

RESULT 3

US-08-938-291A-6
; Sequence 6, Application US/08938291A
; Patent No. 611/673
; GENERAL INFORMATION:
; APPLICANT: Lev, Sima
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: RDBG PROTEINS AND RELATED
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PasteSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,291A
; FILING DATE: September 26, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,337
; FILING DATE: October 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 228/172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 955-0440
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1349 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-938-291A-6

Query Match 9.0%; Score 92; DB 3; Length 1349;
Best Local Similarity 19.3%; Pred. No. 0.51;
Matches 47; Conservative 28; Mismatches 77; Indels 92; Gaps 8;

QY 22 IATWGGDDPKDKLNKESDVSU-----TEDRIILKPGSTPDKL 60
DB 363 IRTKMSNDLMDKIEBPEPEDTQDGLYRQGAPEFRVASSVEQLNITEDVSQPLAAPSRT 422
QY 61 VIDKLVNFG-----NLQEIFTEARTGOENNLGEGKNGVTCFPRP 103
DB 423 HTLLVLHGGTLLDYGADPPSSKKGDANTIANVFPTVRVHYPSALGRLAIRLVPCP--P 480
QY 104 DCP-----LGKSFEEIPVS--PEIPPKSQY-----LRSRMPEG 135
DB 481 VCSDAFALVSNISPSHDEGLSSQDHIPLAALPLATSSFOYGEAVATVQRANLAVG 540
QY 136 TRPEAKQELFSGQ-----SLVPDHCCEGAPNPYLKNSVTAREFLVSEKLPENT 185
DB 541 DFKSQEGMTFNGVCLIGDCVGGILAFDALCYSNQ-----VSESSQSSR 586
QY 186 KGEV 189
DB 587 RGSV 590

RESULT 4

US-09-589-619-6
; Sequence 6, Application US/09589619
; Patent No. 6576442
; GENERAL INFORMATION:
; APPLICANT: Lev, Sima
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Schlessinger, Joseph
; TITLE OF INVENTION: RDBG PROTEINS AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: PasteSeq
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,619
; FILING DATE: 07-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,291
; FILING DATE: September 26, 1997
; APPLICATION NUMBER: 60/027,337
; FILING DATE: October 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 228/172
; TELECOMMUNICATION INFORMATION:

QY 132 -----MPEGRPEAKQQLFSGSLVDPDLCEE 159
Db 236 GTGECTNVSTVQCTHGIRPVVSTQLLNGS-----LAEE 269

RESULT 7
US-07-956-483-12
Sequence 12, Application US/07956483
Patent No. 6261799
GENERAL INFORMATION:
APPLICANT: KIERY, Marie-Paule
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
FILING DATE: 31-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 05392
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feuzy, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 017753-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-956-483-12

Query Match 8.8%; Score 90.5; DB 3; Length 872;
Best Local Similarity 22.3%; Pred. No. 0.4;
Matches 49; Conservative 21; Mismatches 63; Indels 87; Gaps 10;
QY 7 THLCMPVTPNPAESSI--ATWHDGDFKOKLNKESDVSNTEDRIILKPCSTPSDKLVYDK 64
Db 70 THACVPTDNPQEVVLENTENFNMMKNMVEQMHEDIISLWDQSLKPCV-----KLTPLC 123
QY 65 LVVNGNVQLQELFTDEARTG--QENNIGKRGNGVYTCPR-----RPD 104
Db 124 LCVTLN-----CSDELRRNGTGMNNTTEKGMKNSFVNTTVLKDKQGVYALFYRLD 177
QY 105 -----CPGSGFEELPVSPETPPKSGYLRSR----- 131
Db 178 IVDIDDSSTNSNYRLINCNSTSAITQACP-KVSFEPIPIH-YCAPAGFALLKCRDKFN 235
QY 132 -----MPEGRPEAKQQLFSGSLVDPDLCEE 159
Db 236 GTGECTNVSTVQCTHGIRPVVSTQLLNGS-----LAEE 269

RESULT 8
US-08-889-841B-8
Sequence 8, Application US/08889841B
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 486
TYPE: PRT
ORGANISM: HIV
US-08-889-841B-8

Query Match 8.8%; Score 90; DB 3; Length 486;
Best Local Similarity 22.2%; Pred. No. 0.2;
Matches 47; Conservative 20; Mismatches 75; Indels 70; Gaps 7;
QY 7 THLCMPVTPNPAESSI--ATWHDGDFKOKLNKESDVSNTEDRIILKPCSTPSDKLVYDK 64
Db 30 THACVPTDNPQEVVLENTENFNMMKNMVEQMHEDIISLWDQSLKPCV-----KLTPLC 85
QY 65 LVVNGNVQLQELFTDEARTGQENNIGKRGNGVYTCPR----- 102
Db 86 VTLCNTLNENANNNTNNTNNTYTLGEMERGEIKNSFNITSLRDKVKKEVALFYKLDVV 145
QY 103 -----PDCPLKSGFEELPVSPETPPR-----KSGYLRSMP----- 133
Db 146 QIDNSTNYRLISCNSTVITQACP-KVSFEPIPIH-YCAPAGFALLKCRDKKFGTGPCKNV 204
QY 134 -----EGTRPEAKQQLFSGSLVDPDLCEE 159
Db 205 STVQCTHGIRPVVSTQLLNGS-----LAEE 230

RESULT 9
US-09-419-362-8
Sequence 8, Application US/09419362
Patent No. 6585979
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703DIPV
CURRENT APPLICATION NUMBER: US/09/419,362
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: US 08/889,841
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 486
TYPE: PRT
ORGANISM: HIV
US-09-419-362-8

Query Match 8.8%; Score 90; DB 4; Length 486;
Best Local Similarity 22.2%; Pred. No. 0.2;
Matches 47; Conservative 20; Mismatches 75; Indels 70; Gaps 7;
QY 7 THLCMPVTPNPAESSI--ATWHDGDFKOKLNKESDVSNTEDRIILKPCSTPSDKLVYDK 64
Db 30 THACVPTDNPQEVVLENTENFNMMKNMVEQMHEDIISLWDQSLKPCV-----KLTPLC 85
QY 65 LVVNGNVQLQELFTDEARTGQENNIGKRGNGVYTCPR----- 102
Db 86 VTLCNTLNENANNNTNNTNNTYTLGEMERGEIKNSFNITSLRDKVKKEVALFYKLDVV 145

QY 103 -----PDCEPKSFEELPVSPPIPR-----KSOYLRSMP----- 133
DB 146 QIDNSTNYRLISCTSVITQACP-KVSPFELIPHYCAPAGFALKCKDKKFNGTGPKCNV 204
QY 134 -----EGTRPEAKEQLLFSGSLVDPDHCEE 159
DB 205 STVQCTHGIRPVSTQLLNGS-----LAEE 230

RESULT 10

US-09-206-551-11
; Sequence 11, Application US/09206551B
; Patent No. 6521739
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped
; FILE REFERENCE: D6286
; CURRENT APPLICATION NUMBER: US/09/206,551B
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 11
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; OTHER INFORMATION: A_U455 lentiviral env protein
US-09-206-551-11

Query Match 8.5%; Score 86.5; DB 4; Length 855;
Best Local Similarity 24.0%; Pred. No. 1.1;
Matches 47; Conservative 22; Mismatches 70; Indels 57; Gaps 9;

QY 7 THLCWPTVNPASSI--ATWGGDDPKDKLNKESDSVNTEDRLKPC--STP--SDKLV 61
DB 69 THACVPTDNPGEIDLVNVTSEFNWKNMVDQMEDIISLMDQSLKPCVKLTPLCVTL 128
QY 62 IDKLNVNFGNVLOEFTDEARTQEN-----NLGEGKNGVYTCPPRPD----- 104
DB 129 CHNITINNTNNNTNI--TDGVREEMKNCFSNMTTELRDKQKXVSLFYRDIYQINKTDNN 187
QY 105 -----CPLKSPFELPVSPPIPRKSOYLRSMP----- 134
DB 188 SYRLINCNTSTTQACP-KVSPFELIPHY-YCAPAGFALKCKDKPEFNKGPCPNVSTVQC 245
QY 135 --GTRPEAKEQLLFSG 148
DB 246 THGIRPVSTQLLNG 261

RESULT 11
US-09-206-551-12
; Sequence 12, Application US/09206551B
; Patent No. 6521739
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice H.
; APPLICANT: Gao, Feng
; APPLICANT: Marx, Preston A.
; APPLICANT: Shaw, George M.
; APPLICANT: Smith, Stephen M.
; APPLICANT: Georges-Courbot, Marie Claude
; APPLICANT: Lu, Chang Yong
; TITLE OF INVENTION: Complete Genome Sequences of a Simian
; TITLE OF INVENTION: Immunodeficiency Virus from a Red-Capped

; TITLE OF INVENTION: Mangabey
; FILE REFERENCE: D6286
; CURRENT APPLICATION NUMBER: US/09/206,551B
; CURRENT FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 12
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Simian immunodeficiency virus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of homologous region of
; OTHER INFORMATION: B_HXB2R lentiviral env protein
US-09-206-551-12

Query Match 8.5%; Score 86.5; DB 4; Length 855;
Best Local Similarity 24.0%; Pred. No. 1.1;
Matches 47; Conservative 22; Mismatches 70; Indels 57; Gaps 9;

QY 7 THLCWPTVNPASSI--ATWGGDDPKDKLNKESDSVNTEDRLKPC--STP--SDKLV 61
DB 69 THACVPTDNPGEIDLVNVTSEFNWKNMVDQMEDIISLMDQSLKPCVKLTPLCVTL 128
QY 62 IDKLNVNFGNVLOEFTDEARTQEN-----NLGEGKNGVYTCPPRPD----- 104
DB 129 CHNITINNTNNNTNI--TDGVREEMKNCFSNMTTELRDKQKXVSLFYRDIYQINKTDNN 187
QY 105 -----CPLKSPFELPVSPPIPRKSOYLRSMP----- 134
DB 188 SYRLINCNTSTTQACP-KVSPFELIPHY-YCAPAGFALKCKDKPEFNKGPCPNVSTVQC 245
QY 135 --GTRPEAKEQLLFSG 148
DB 246 THGIRPVSTQLLNG 261

RESULT 12
US-09-252-991A-26008
; Sequence 26008, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26008
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26008

Query Match 8.5%; Score 86; DB 4; Length 423;
Best Local Similarity 31.9%; Pred. No. 0.44;
Matches 30; Conservative 15; Mismatches 33; Indels 16; Gaps 5;

QY 12 PVPV-NPAESSIATWGGDDPKDKLNKESDSVNTEDRLKCPSPDKLVTDKLVNFG 70
DB 22 PTFPESVADGTVAITH-----KRGKGVKXDELIV--DIETDKVILEVLAADG 68
QY 71 NVLOEIFTDEARTQENNLGEGKNGVYTCPPRP 103
DB 69 -VLAELIKKNGDPTVLSNELGLNKGAAAPAP 101

RESULT 13
US-07-956-483-14
; Sequence 14, Application US/07956483


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Db      31 THACVPTDNPQEIIELVN-VTDEDFNMKKKKKMDQGHEDDIIISLMBELKPCVLTPLCLCYTL 89
QY      54 -----STPESDKLVIDKLNVNFGVNLQEIPTDEARTQGENNLGGEKNGGYVTCPPR--- 102
           :  :  :
Db      90 NCSDVNNSTNPND-----TNTNSTNTTTSPTPTATTSSEKK--EKGIKKCSFNITTT 139
           :  :  :
QY      103 -----PDCPLGKSFEEELPVSPPELP-- 121
           :  :  :
Db      140 HMKDKVQKEVALFYKLDIVPIDDNNNTSYRLISCNSTSVITQACSM-VTFEPIPIHYCAPAG 198
QY      122 -----PRK-----SOLYLRSMEEGTRPEAKQELTFSGQSLVDPDHLCEE 159
           :  :  :
Db      139 FALIKCKDKKFFNGTGFCSCSKVSTYVQCHTHGRIPVSVTQDLLNGS-----LAEE 244

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OM protein - protein search, using sw model

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(without alignments)
1002.770 Million cell updates/sec

Title: US-09-892-949-2_COPY_544_732

Perfect score: 1017
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Scoring table: BLOSUM62
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Searched: 492763 seqs, 131003257 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Published_Applications_AA.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1017	100.0	732	11	US-09-892-949-2	Sequence 2, Appli
2	1010	99.3	745	11	US-09-972-708-4	Sequence 4, Appli
3	514.5	50.6	649	11	US-09-892-949-46	Sequence 46, Appli
4	514.5	50.6	662	11	US-09-972-708-15	Sequence 15, Appli
5	514.5	50.6	662	11	US-09-892-949-54	Sequence 54, Appli
6	514.5	50.6	662	15	US-10-006-265-17	Sequence 17, Appli
7	483.5	47.5	726	11	US-09-972-708-12	Sequence 12, Appli
8	462	45.4	652	11	US-09-972-708-14	Sequence 14, Appli
9	462	45.4	652	15	US-10-006-265-2	Sequence 2, Appli
10	304	29.9	652	11	US-09-892-949-57	Sequence 57, Appli
11	95.5	9.4	854	12	US-10-190-435-5	Sequence 5, Appli
12	95.5	9.4	854	12	US-10-190-435-128	Sequence 128, App
13	91.5	9.0	619	10	US-09-891-609-4	Sequence 4, Appli
14	91.5	9.0	646	10	US-09-891-609-2	Sequence 2, Appli
15	88.5	8.7	865	12	US-10-190-435-140	Sequence 140, App

16	86.5	8.5	803	12	US-10-190-435-134	Sequence 134, App
17	86.5	8.5	803	12	US-10-190-435-135	Sequence 135, App
18	86	8.5	503	9	US-09-759-841-4	Sequence 4, Appli
19	85.5	8.4	1258	10	US-09-922-543-1	Sequence 1, Appli
20	84.5	8.3	858	12	US-10-190-435-150	Sequence 150, App
21	83.5	8.2	853	12	US-10-286-332A-33	Sequence 33, App
22	83.5	8.2	853	14	US-10-003-035-33	Sequence 33, Appli
23	83.5	8.2	903	11	US-09-746-783-142	Sequence 142, App
24	83.5	8.2	1101	12	US-10-286-332A-53	Sequence 53, Appli
25	83.5	8.2	1101	14	US-10-003-035-53	Sequence 53, Appli
26	83.5	8.2	1186	12	US-10-286-332A-55	Sequence 55, Appli
27	83.5	8.2	1186	14	US-10-003-035-55	Sequence 55, Appli
28	83	8.2	511	9	US-09-864-761-34590	Sequence 34590, A
29	82.5	8.1	579	15	US-10-032-162-15	Sequence 15, Appli
30	82.5	8.1	790	15	US-09-765-519-2	Sequence 2, Appli
31	82.5	8.1	849	15	US-10-235-994-2	Sequence 2, Appli
32	82.5	8.1	799	12	US-10-190-435-148	Sequence 148, App
33	82.5	8.1	862	12	US-10-190-435-141	Sequence 141, App
34	82.5	8.1	869	12	US-10-190-435-4	Sequence 4, Appli
35	82.5	8.1	870	12	US-10-190-435-127	Sequence 127, App
36	82	8.1	506	10	US-09-934-060A-24	Sequence 24, Appli
37	82	8.1	506	10	US-09-934-060A-30	Sequence 30, Appli
38	82	8.1	556	10	US-09-934-060A-6	Sequence 6, Appli
39	82	8.1	720	10	US-09-934-060A-2	Sequence 2, Appli
40	82	8.1	720	10	US-09-934-060A-4	Sequence 4, Appli
41	82	8.1	1080	9	US-09-904-380-2	Sequence 2, Appli
42	81	8.0	100	15	US-10-032-162-2	Sequence 2, Appli
43	81	8.0	502	9	US-09-796-202-16	Sequence 16, Appli
44	81	8.0	502	12	US-10-323-314-16	Sequence 16, Appli
45	81	8.0	625	15	US-10-032-162-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-09-892-949-2
; Sequence 2, Application US/09892949
; Publication No. US20030096339A1
GENERAL INFORMATION:
; APPLICANT: Sprenger, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-2
Query Match 100.0%; Score 1017; DB 11; Length 732;
Best Local Similarity 100.0%; Pred. No. 4.8e-97;
Matches 189; Conservative 0; Indels 0; Gaps 0;
QY 1 KKPNTLTHLCPVTVPNPAESATWHDGDFDKLTKSSDSVYNEEDILKPCSPDKL 60
DB 544 KKPNTLTHLCPVTVPNPAESATWHDGDFDKLTKSSDSVYNEEDILKPCSPDKL 603
QY 61 VIDKLIVNFGVNLQRIFTDEARTGQENNLGGEKNGYVTCPPRPDCLPKSFEELPVSPDI 120

DB 604 VIDKLIVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 663
QY 121 PPKRSQYLRSRMPEGTRPEAKESQSLVDPDHLCEBGAHPNYLKNSTAREFLVSEK 180
DB 664 PPKRSQYLRSRMPEGTRPEAKESQSLVDPDHLCEBGAHPNYLKNSTAREFLVSEK 723
QY 181 LPEHTKGEV 189
DB 724 LPEHTKGEV 732

RESULT 2

US-09-972-708-4
; Sequence 4, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-4

Query Match 99.3%; Score 1010; DB 11; Length 745;
Best Local Similarity 99.5%; Pred. No. 2.6e-96;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKPKNLTLHCWPTVNPAPASSIATWGGDDPKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
DB 557 KKPKNLTLHCWPTVNPAPASSIATWGGDDPKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616
QY 61 VIDKLIVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 120
DB 617 VIDKLIVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 676
QY 121 PPKRSQYLRSRMPEGTRPEAKESQSLVDPDHLCEBGAHPNYLKNSTAREFLVSEK 180
DB 677 PPKRSQYLRSRMPEGTRPEAKESQSLVDPDHLCEBGAHPNYLKNSTAREFLVSEK 736
QY 181 LPEHTKGEV 189
DB 737 LPEHTKGEV 745

RESULT 3

US-09-892-949-46
; Sequence 46, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prensell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26

; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-46

Query Match 50.6%; Score 514.5; DB 11; Length 649;
Best Local Similarity 94.2%; Pred. No. 8.3e-45;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPKNLTLHCWPTVNPAPASSIATWGGDDPKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
DB 544 KKPKNLTLHCWPTVNPAPASSIATWGGDDPKDKLNKESDSDSVNTEDRILKPCSTPSDKL 603
QY 61 VIDKLIVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 100
DB 604 VIDKLIVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 646

RESULT 4

US-09-972-708-15
; Sequence 15, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-15

Query Match 50.6%; Score 514.5; DB 11; Length 662;
Best Local Similarity 94.2%; Pred. No. 8.5e-45;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPKNLTLHCWPTVNPAPASSIATWGGDDPKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
DB 557 KKPKNLTLHCWPTVNPAPASSIATWGGDDPKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616
QY 61 VIDKLIVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 100
DB 617 VIDKLIVNFGNVLOEIFTDEARTGOENNLGGEKNGVYTCFPRDCELGKSFEEELPVSPET 659

RESULT 5

US-09-892-949-54
; Sequence 54, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Prensell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurel, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17

FILE REFERENCE: 00-42
CURRENT APPLICATION NUMBER: US/09/892,949
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,282
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,955
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/267,963
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FastSeq for windows Version 3.0
SEQ ID NO 54
LENGTH: 662
TYPE: PRT
ORGANISM: Homo sapiens
US-09-892-949-54

Query Match 50.6%; Score 514.5; DB 11; Length 662;
Best Local Similarity 94.2%; Pred. No. 8.5e-45;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
DB 557 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616
QY 61 VIDKLVNFGNVLQEIFTDEARTGOENNLGEGKNG--YVTCG 100
DB 617 VIDKLVNFGNVLQEIFTDEARTGOENNLGEGKNGRIIISSCP 659

RESULT 6
US-10-006-265-17
Sequence 17, Application US/1006265
Publication No. US20030125520A1
GENERAL INFORMATION:
APPLICANT: Maeda, Masatsugu
APPLICANT: Yaguchi, No. US20030125520A1iko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
FILE REFERENCE: 06501-096001
CURRENT APPLICATION NUMBER: US/10/006,265
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/JP00/03556
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: JP 11/155797
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: JP 11/217797
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for windows Version 4.0
SEQ ID NO 17
LENGTH: 662
TYPE: PRT
ORGANISM: Homo sapiens
US-10-006-265-17

Query Match 50.6%; Score 514.5; DB 15; Length 662;
Best Local Similarity 94.2%; Pred. No. 8.5e-45;
Matches 97; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
DB 557 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616
QY 61 VIDKLVNFGNVLQEIFTDEARTGOENNLGEGKNG--YVTCG 100
DB 617 VIDKLVNFGNVLQEIFTDEARTGOENNLGEGKNGRIIISSCP 659

RESULT 7
US-09-972-708-12
Sequence 12, Application US/09972708
Publication No. US20030059871A1
GENERAL INFORMATION:

APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 726
TYPE: PRT
ORGANISM: Mus musculus
US-09-972-708-12

Query Match 47.5%; Score 483.5; DB 11; Length 726;
Best Local Similarity 56.0%; Pred. No. 1.6e-41;
Matches 107; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 1 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
DB 541 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 597
QY 61 VIDKLVNFGNVLQEIFTDEARTGOENNLGEGKNGVTCPPRPPDCLGKSPFELVSPER 120
DB 598 LIDKLVNFGNVLQEIFTDEARTGOENNLGEGKNGVTCPPRPPDCLGKSPFELVSPER 657
QY 121 PPKSQYLRSNPECTREPAKEQLIFSGOS--LYVDHLCEGAPNPYLNKSVTAREFLVS 178
DB 658 ASEDSHSTCSRADAVSELRARQPSGSCQPSLSPPR--EDQAQNPYLNKSVTAREFLVS 715
QY 179 EKLPHHTGGEV 189
DB 716 ENIPHSKGEV 726

RESULT 8
US-09-972-708-14
Sequence 14, Application US/09972708
Publication No. US20030059871A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Cosman, David J.
APPLICANT: Mosley, Bruce A.
APPLICANT: Bird, Timothy A.
APPLICANT: Dubose, Robert F.
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
FILE REFERENCE: 3160-B
CURRENT APPLICATION NUMBER: US/09/972,708
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 652
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-708-14

Query Match 45.4%; Score 462; DB 11; Length 652;
Best Local Similarity 100.0%; Pred. No. 2.4e-39;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 60
DB 557 KKPKNLTLHCWPTVPNPASSIATWGHGDDFKDKLNKESDSDSVNTEDRILKPCSTPSDKL 616
QY 61 VIDKLVNFGNVLQEIFTDEARTGOE 86
DB 617 VIDKLVNFGNVLQEIFTDEARTGOE 642

RESULT 9

US-10-006-265-2
; Sequence 2, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006, 265
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-2

Query Match 45.4%; Score 462; DB 15; Length 652;
Best Local Similarity 100.0%; Pred. No. 2,4e-39;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKKNKTLTLCMPVPNPASSIATWGGDFDKDLNKESDVSNTDRILKPCSTPSDKL 60
DB 557 KKKNKTLTLCMPVPNPASSIATWGGDFDKDLNKESDVSNTDRILKPCSTPSDKL 616
QY 61 VIDKLNVNFGNVLQEIFTDARTGQE 86
DB 617 VIDKLNVNFGNVLQEIFTDARTGQE 642

RESULT 10

US-09-892-949-57
; Sequence 57, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuljper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892, 949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 662
; TYPE: PRT
; ORGANISM: mus musculus
US-09-892-949-57

Query Match 29.9%; Score 304; DB 11; Length 662;
Best Local Similarity 58.5%; Pred. No. 6,9e-23;
Matches 62; Conservative 14; Mismatches 26; Indels 4; Gaps 3;

QY 1 KKKNKTLTLCMPVPNPASSIATWGGDFDKDLNKESDVSNTDRILKPCSTPSDKL 60
DB 558 KKKNKTLTLCMPVPNPASSIATWGGDFDKDLNKESDVSNTDRILKPCSTPSDKL 614
QY 61 VIDKLNVNFGNVLQEIFTDARTGQENNLGKNGYVTCPPDPCE 106
DB 615 VIDKLNVNFGNVLQEIFTDARTGQENNLGKNGYVTCPPDPCE 659

RESULT 11

US-10-190-435-5
; Sequence 5, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TV2.12-5/1
US-10-190-435-5

Query Match 9.4%; Score 95.5; DB 12; Length 854;
Best Local Similarity 22.3%; Pred. No. 0.5;

Matches 52; Conservative 26; Mismatches 76; Indels 79; Gaps 13;

QY 7 TLLCWPVPNPAPAE-----SIAATWGGDFDKDLNKESDVSNTDRILKPC--STP- 56
DB 69 TLLCWPVPNPAPAE-----SIAATWGGDFDKDLNKESDVSNTDRILKPC--STP- 123
QY 57 SDKLVIDKLNVNFGNVLQEI-----FTDEARTGQENN-----LGKNGYV-- 97
DB 124 CVTLNCTATVYNNNTSDMKKCSFYVTELDKDKKENALFYRLDIYPLNNRKGNN 183
QY 98 -----TCTPRPDPLGKSGFEELVSPERIP---PKTSQYLR-----SRMPE 134
DB 184 YRLNCTNSATYQACP-KVSPDPIPIHYCAPAGVAPLKNMKKFGIGPCDVSIVQCTH 242
QY 135 GTRPEAKGQLPFGSGSLVVDHLCGAGNPVYKNSVTAREFLV-SEKLPEHTK 186
DB 243 GIKPVVSTQLLNG-----SLAEERITIRSENLTNNYK 275

RESULT 12

US-10-190-435-128
; Sequence 128, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; PRIOR FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 128

LENGTH: 854
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TV002c12.1
US-10-190-435-128

Query Match
Best Local Similarity 22.3%; Pred. No. 0.5;
Matches 52; Conservative 26; Mismatches 76; Indels 79; Gaps 13;

QY 7 TLHCWTVNPAE-----SSIAWGGDDFKDLNKLKESDVSNTEDRIKPC--STP- 56
DB 69 THACVPTDNPDEIVLENTENFNMMK--NDVWDQ-----QEDIIISLMDQSLKPCVLTPL 123
QY 57 SDKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 97
DB 124 CCTLNCTNATVNNNTSKMKKCSFYVTTLMDKKKKENALPRLDIVFLNKKNNIN 183
QY 98 -----TCPRPDCPLGKSFELPVSPRIP--PRKSQYLR-----SRMPE 134
DB 184 YRLINCNATSAIQACP-KVSFDPRIHYCAPAGYAPLCKNNKKFNGIGPCDNVSTVQCTH 242
QY 135 GTRPEAKQLFSGQSLVDPDLCEBAGAPRYLKNSVTAREFLV-SEKLPENHTK 186
DB 243 GIKPVVSTQLLNG-----SLAEEELIIRSENLTNNYK 275

RESULT 13
US-09-891-609-4
Sequence 4, Application US/09891609
Patent No. US20020127238A1
GENERAL INFORMATION:
APPLICANT: Stamatacos, Leonidas
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
FILE REFERENCE: 2570-1-002N
CURRENT APPLICATION NUMBER: US/09/891,609
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,608
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 619
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-891-609-4

Query Match
Best Local Similarity 24.9%; Pred. No. 0.83;
Matches 47; Conservative 23; Mismatches 66; Indels 53; Gaps 10;

QY 7 TLHCWTVNPAESSI--ATWGGDDFKDLNKLKESDVSNTEDRIKPC--STP- 62
DB 43 THACVPTDNPDEIVLENTENFNMMK--NDVWDQ-----QEDIIISLMDQSLKPCVLTPL 99
QY 63 DKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 107
DB 100 TLHCWTVNPAESSI--ATWGGDDFKDLNKLKESDVSNTEDRIKPC--STP- 150
QY 108 GKSFEELPVSPRIP--PRK-----SOYLRSRMEGTRPEAKQLFSGQSL 151
DB 151 KVSFDPRIHYCAPAGYAPLCKNNKKFNGIGPCDNVSTVQCTH 208
QY 152 VPDHLCERG 160
DB 209 ---LAERG 213

RESULT 14
US-09-891-609-2
Sequence 2, Application US/09891609
Patent No. US20020127238A1

GENERAL INFORMATION:
APPLICANT: Stamatacos, Leonidas
TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
FILE REFERENCE: 2570-1-002N
CURRENT APPLICATION NUMBER: US/09/891,609
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,608
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 646
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-891-609-2

Query Match
Best Local Similarity 24.9%; Pred. No. 0.88;
Matches 47; Conservative 23; Mismatches 66; Indels 53; Gaps 10;

QY 7 TLHCWTVNPAESSI--ATWGGDDFKDLNKLKESDVSNTEDRIKPC--STP- 62
DB 70 THACVPTDNPDEIVLENTENFNMMK--NDVWDQ-----QEDIIISLMDQSLKPCVLTPL 126
QY 63 DKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 107
DB 127 TLHCWTVNPAESSI--ATWGGDDFKDLNKLKESDVSNTEDRIKPC--STP- 177
QY 108 GKSFEELPVSPRIP--PRK-----SOYLRSRMEGTRPEAKQLFSGQSL 151
DB 178 KVSFDPRIHYCAPAGYAPLCKNNKKFNGIGPCDNVSTVQCTH 235
QY 152 VPDHLCERG 160
DB 236 ---LAERG 240

RESULT 15
US-10-190-435-140
Sequence 140, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 140
LENGTH: 865
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TV008c4.3
US-10-190-435-140

Query Match
Best Local Similarity 24.7%; Pred. No. 2.7;
Matches 38; Conservative 21; Mismatches 48; Indels 47; Gaps 8;

QY 7 TLHCWTVNPAE-----SSIAWGGDDFKDLNKLKESDVSNTEDRIKPCSTPSDK 59
DB 70 THACVPTDNPDEIVLENTENFNMMK--NDVWDQ-----QEDIIISLMDQSLKPCVLTPL 120
QY 60 LVIDKLIVNFGVNLQEI-----FTDEARTGOENN-----LGGKNGYV-- 119
DB 121 LTPCLVTLNCSVIVSNVTNTVT--HNNT--TDKEMNCTFN-----ITTE 164

Qy 120 IPPKSOYLRSRMPEGTREPEAKEOLPFGQSLVP 153
Db 165 ITDKS-----KEYATFYRLDVP 183

Search completed: August 18, 2003, 13:33:23
Job time : 26.0245 secs

Db 104 CTDNMGN-----YTVKRRNVTSGGEMKEMKGN-----CSF 134

RESULT 6

T33172 hypothetical protein M01B12.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T33172

R:Becker, M.; Graves, T.; Ozersky, P.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid M01B12.

A:Reference number: 221297

A:Accession: T33172

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-548 <BEC>

A:Cross-references: EMBL:AF067624; PIDN:AC17564.1; GSPDB:GN00019; CESP:M01B12.5

A:Genetics:

A:Gene: CESP:M01B12.5

A:Map position: 1

A:Intons: 39/1; 70/1; 94/1; 122/3; 190/2; 260/2; 301/3; 372/2

Query Match 8.5%; Score 86.5; DB 2; Length 548;
Best Local Similarity 26.6%; Pred. No. 7.2;
Matches 50; Conservative 29; Mismatches 78; Indels 31; Gaps 9;

QY 15 PNPASSIAT--WHGDDFKDLNLEKSDSVN-TEDRIKFCSTPSPDKLVNFK 70

Db 85 PNAANRRLVDVERHADTSEDRKRKVRADRAVEQVL---DPRTLVFRLLQR-G 139

QY 71 NVLQGE---LFTDEA-----RTGQENNLG-----GKNGVYTCFPRDCLGKSF 111

Db 140 TILNIDGCISTGEANVYHATGNDLAIKIYKTSILTFKDBRYVTGFRFRHGYCKSN 199

QY 112 EELPVSPEIPPKSQYLSPMEGTRPEAKEQLLFSGOSLVDPDHLCEBAPNPYLKNSVT 171

Db 200 PRKMYA--VMAEKEMRNILARMEHVGLPVRKPHLL-KGHVLVNDPLGKDCMPAPLKNAL 256

QY 172 ABEPLVSE 179

Db 257 SQEVAISK 264

RESULT 7

H83448 dihydrolipoamide succinyltransferase (B2 subunit) PA1586 [imported] - Pseudomonas aerugi-

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: H83448

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br-

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lam,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83448

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-409 <STO>

A:Cross-references: GB:AE004586; GB:AE004091; NID:g9947536; PIDN:AA04975.1; GSPDB:GN001

A:Experimental source: strain PA01

A:Genetics:

A:Gene: sucB; PA1586

C:Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match 8.5%; Score 86; DB 2; Length 409;

Best Local Similarity 31.9%; Pred. No. 5.4;

Matches 30; Conservative 15; Mismatches 33; Indels 16; Gaps 5;

QY 12 PTPV-NPASESIATWHGDDFKDLNLEKSDSVNTEDRILKFCSTPSPDKLVNFK 70

Db 8 PTFPESVADGTVATWH-----KKRGAVKRDELIV---DIETKVVLEVLAADG 54

QY 71 NVLQGEIIFDEARTGQENNLGGEKN-GYVTCFPR 103

Db 55 -VLAIEIINKEGDTVLISNELLGKLNKGAAAPAP 87

env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N:Alternate names: coat polyprotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C:Accession: J00066

R:Spire, B.; Site, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;

Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the human immunc

A:Reference number: J00065; MUID:90034200; PMID:2806917

A:Accession: J00066

A:Molecule type: DNA

A:Residues: 1-846 <SPI>

A:Cross-references: GB:M27323; NID:G328154; PIDN:AAA44873.1; PID:G328162

A:Note: the authors translated the codon GCG for residue 523 as Arg

C:Genetics:

A:Gene: env

C:Superfamily: type B retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

F.1-29/Domain: signal sequence #status predicted <SIG>

F.30-501/Product: coat protein gp120 #status predicted <CP1>

F.502-846/Product: coat protein gp41 #status predicted <CP2>

F.674-692/Domain: transmembrane #status predicted <TM2>

F.87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606

Query Match 8.5%; Score 86; DB 1; Length 846;

Best Local Similarity 20.2%; Pred. No. 14;

Matches 49; Conservative 23; Mismatches 74; Indels 96; Gaps 9;

QY 7 THLCMPVTPNPASSI--ATWHGDDFKDLNLEKSDSVNTEDRILKFCSTPSPDKLVNFK 64

Db 70 THACVPTDPNPDEILEVNTENFMNWKNNVGEQMHEDIISLMDQSLKXC-----VKLTP 123

QY 65 LVVNFQNVQLFETDEARTGQENNLGGEKNGYVTCPR----- 102

Db 124 LCVTLN-----CTDELNNSKNGKRVBEERKKNCSFVNRDRREQVALFYKLDIVPIDN 177

QY 103 -----PDCLPGKSFEEIPVSPRIIPKRSQYLRSR----- 131

Db 178 NNRNTSTVRLINCSTSTITGQAC-KISFEPLPIH-PCAPAGFALKRDKKFNQTGPCS 235

QY 132 -----MDEGTRPEAKEQLLFSGOSLVDPDHLCEBAPNPYLKNSVTAREFLV-SKLPDEH 184

Db 236 NVSTVQCTHGIRPVVSTQLLNG-----SLAEEIIRSNLNN 275

QY 185 TK 186

Db 276 VK 277

RESULT 9

S54384 envelope polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C:Accession: S54384

R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377

A:Accession: S54384

A:Status: preliminary

RESULT 13
A:Species: B-lymphocyte-induced maturation protein 1 - mouse
N:Alternate names: Blimp-1
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C:Accession: A53503
R:Turner Jr., C.A.; Mack, D.H.; Davis, M.M.
Cell 77, 297-306, 1994
A>Title: Blimp-1, a novel zinc finger-containing protein that can drive the maturation of B-lymphocytes
A:Reference number: A53503; MID:94221646; PMID:8168136
A:Accession: A53503
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-856 <TUR>
A:Cross-references: GB:U08185; NID:9474283; PIDN:AAA19252.1; PID:9474284
C:Keywords: transcription factor; zinc finger

Query Match 8.3%; Score 84; DB 2; Length 856;
Best Local Similarity 22.1%; Pred. No. 22;
Matches 43; Conservative 33; Mismatches 81; Indels 38; Gaps 9;
QY 15 PNPASISATWHDHDKDKL-----NKKESDSDS---VNTEDRLKPCSTSDKL 60
DB 221 PTPANQELLVWYCRDFAERLHYPPEGLTVINLTQESNPKOYSSKNELYPKSVPKREY 280
QY 61 VIDKLAVNFGN--VLQEIFTDEAR--TGQENNIGKKNQVYTCPPRP-----DCPLGKS 110
DB 281 SVKEILKDSNPKKDIYRSNISPTLEKMDGFRKNSPMPFYPRVYVYPRALPES 340
QY 111 FEELVPSPEIPPRKSOYL-RSRMEGTRPEAKQQLFSGQSLVDPHLCEGADNPYLKNS 169
DB 341 F-LKSLAVGMERPHYTHSPSPSTTSPSP-----ASSPEQSLKSSSPHSPGWT 391
QY 170 VTRAREPLVSEKLEPH 184
DB 392 VSP---LAPGLEPH 402

RESULT 14
JC6121
transcription factor Pit-1 - chinook salmon
N:Alternate names: transcription factor GHF-1
C:Species: Oncorhynchus tshawytscha (chinook salmon)
C>Date: 22-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: JC6121; A41928
R:Maumdar, S.; Irwin, D.M.; Elsholtz, H.P.
Proc. Natl. Acad. Sci. U.S.A. 93, 10256-10261, 1996
A>Title: Selective constraints on the activation domain of transcription factor Pit-1.
A:Reference number: JC6121; MID:96413633; PMID:8816787
A:Accession: JC6121
A:Molecule type: mRNA
A:Residues: 1-358 <MAJ>
A:Cross-references: GB:U05045; NID:91621540; PIDN:AAI17254.1; PID:91621541
R:Elsholtz, H.P.; Maumdar-Somlyai, S.; Xiong, F.; Gong, Z.; Hew, C.L.
Mol. Endocrinol. 6, 515-522, 1992
A>Title: Phylogenetic specificity of prolactin gene expression to conservation of Pit-1
A:Reference number: A41928; MID:92261606; PMID:1350055
A:Accession: A41928
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 198-341 <EL>
C:Genetics:
A:Gene: pit-1
C:Superfamily: transcription factor Pit-1; homeobox homology; POU domain homology
C:Keywords: DNA binding; homeobox; nucleus; pituitary; transcription regulation
F:199-266/Domain: POU domain homology <POU>
F:283-339/Domain: homeobox homology <HOX>

Query Match 8.2%; Score 83.5; DB 1; Length 358;
Best Local Similarity 25.3%; Pred. No. 7.7;
Matches 42; Conservative 15; Mismatches 58; Indels 51; Gaps 7;

QY 45 TEDRLKPCSTPSPDKLVIDKLAVNFGNVLQEIFTDEARTQENNIGKKNQVYTCPPRPD 104
DB 110 SQRILLQTCVSHPHNM-----VNGANTLQGSILAPCLYKQEHGIG-----GS 152
QY 105 CPLGKSFPELP---VSPPEIP--PRKSQYLRSMRPG-----TRPEAKQQLFS----- 147
DB 153 CSLSHSPPLPPAVLSESPPLGKNDRLRSSRPDPDPNMDSPQIRLEKPFANDFKLRRI 212
QY 148 -----GQSLVDPH-----LCEGAPNPYLKNSVTRAREPL 176
DB 213 KLGQYQTVNGEALAAVHGSFSGQTTCRPNQLSFKACTIKALT 258

RESULT 15
VCPV2
coat protein VP1 - parvovirus H1
C:Species: parvovirus H1
A>Note: host Homo sapiens (man)
C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 08-Apr-1994
C:Accession: A03699
R:Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A>Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybridization
A:Reference number: A03699; MID:83112183; PMID:6823009
A:Accession: A03699
A:Molecule type: DNA
A:Residues: 1-722 <RNA>
A:Cross-references: EMBL:X01457; EMBL:J02198
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 8.2%; Score 83.5; DB 1; Length 722;
Best Local Similarity 20.8%; Pred. No. 19;
Matches 43; Conservative 25; Mismatches 82; Indels 57; Gaps 8;
QY 4 NKLTLCPPTVNPASSI---ATWGDDEKDKLNKESDSDSVNTEDRLKPCS----- 54
DB 197 SRLHLGMPSENYCRVTVHNNQTTGHGTVKXGNN-----AYDTHQQLWTPMGLVDAN 249
QY 55 -----TPSDKLVIDKLAV--VNFQNVVLQEIFTDEARTQENNIGK-----KNGVVC- 99
DB 250 AMGVWFQPSDWQFQNSMESLNDLSQLEFNVVVKVTEQOQAGQDAIKYNNNDLTKCM 309
QY 100 -----PRPDCCPLGKSFPELPVSPPEIP-----PRKSQYLRSMRPG----- 137
DB 310 MWALDSNNILPPTPAQGSSETIGFYPMKPTAPAPYRYFFMPRQLSTVSSNABSTQITD 369
QY 138 -----PEAKQQLFSGQSLVDPHLCEEG 160
DB 370 TIGBPQALNSQFTIENTLPTILRTG 396

Search completed: August 18, 2003, 13:31:22
Job time: 27.4869 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:27 ; Search time 14.3658 Seconds
(without alignments)
618.695 Million cell updates/sec

Title: US-09-892-949-2_COPY_544_732
Perfect score: 1017
Sequence: 1 KKKNNKLTLLCWPTEVPNPAES.....VTAREFLVSEKLPHTKGEV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96.5	9.5	856	ENV_HV1ZH	P05881 human immun
2	93	9.1	918	IL6B_RAT	P40190 rattus norv
3	92	9.0	250	HXB9_HUMAN	P17482 homo sapien
4	90.5	8.9	853	ENV_HV1EL	P04581 human immun
5	90.5	8.9	867	ENV_HV1J3	P12489 human immun
6	86	8.5	846	ENV_HV1ND	P18799 human immun
7	86	8.5	853	ENV_HV1Z2	P12487 human immun
8	85	8.5	856	ENV_HV1SC	P05878 human immun
9	85	8.4	380	TGT_CLOPE	O8XJ16 clostridium
10	84	8.3	856	PRDI_MOUSE	O60636 mus musculu
11	83.5	8.2	722	COAT_PAVHH	P03136 hamster par
12	83	8.2	852	ENV_HV1S3	P19549 human immun
13	82.5	8.1	790	TNP3_HUMAN	P21580 homo sapien
14	82.5	8.1	853	ENV_HV1MF	P19551 human immun
15	82.5	8.1	861	ENV_HV1KB	P31819 human immun
16	82.5	8.1	917	IL6B_MOUSE	O00560 mus musculu
17	81.5	8.0	358	PIT1_ONCMY	O08478 oncorhynch
18	81.5	8.0	365	PIT1_ONCKE	O91169 oncorhynch
19	81.5	8.0	855	ENV_HV1Z6	P04580 human immun
20	81	8.0	709	SHPI_RAT	O92569 rattus norv
21	80.5	7.9	855	ENV_HV1OY	P20888 human immun
22	80	7.9	467	INVO_MOUSE	P48997 mus musculu
23	80	7.9	709	SHPI_MOUSE	O87550 mus musculu
24	80	7.9	836	GCGR_HUMAN	O99062 homo sapien
25	80	7.9	861	ENV_HV1BR	P03377 human immun
26	79	7.8	848	ENV_HV1JR	P20871 human immun
27	79	7.8	1562	YFRD_SCHPO	O9ut43 schizosacch
28	78	7.7	590	MSP_TRELE	O8rmc0 treponema 1
29	78	7.7	665	SHPI_HUMAN	O96b97 homo sapien
30	78	7.7	847	ENV_HV1S1	P19550 human immun
31	78	7.7	856	ENV_HV1W1	P31872 human immun
32	78	7.7	960	YMX6_YEAST	O04279 saccharomyc
33	77.5	7.6	379	PROB_VIBVU	O8df93 vibrio vuln

34	77.5	7.6	1270	1	ITN1_XENLA	O42287 xenopus lae
35	77	7.6	626	1	TES1_HUMAN	O15569 homo sapien
36	77	7.6	847	1	ENV_HV1W2	P05880 human immun
37	76	7.5	846	1	MAK5_HUMAN	O9Y4K4 homo sapien
38	76	7.5	892	1	YLB3_CAEEL	P46578 caenorhabdi
39	75.5	7.4	851	1	ENV_HV1B8	P04582 human immun
40	75.5	7.4	3396	1	PGCV_HUMAN	P13611 homo sapien
41	75	7.4	421	1	ENV_HV1NS	P12490 human immun
42	75	7.4	789	1	PRDI_HUMAN	O75626 homo sapien
43	75	7.4	843	1	ENV_HV1Y2	P35961 human immun
44	75	7.4	863	1	ENV_HV1Z8	P05882 human immun
45	75	7.4	1637	1	MSPF_STAAU	P80544 staphylococ

ALIGNMENTS

RESULT 1	ID	ENV_HV1ZH	STANDARD;	PRT;	856 AA.
AC	P05881;				
DT	01-NOV-1988 (Rel. 09, Last sequence update)				
DT	01-NOV-1988 (Rel. 09, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (Zaire H3321 isolate) (HIV-1).				
OC	Viruses; Retroviridae; Retroviridae; Lentiviridae.				
OX	NCBI_Taxid=11692;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8922876; PubMed=2713163;				
RA	Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getchell J., McCormick J., Ou C.Y., Myers G., Smith T., Chen E.,				
RA	"Molecular characterization of HIV-1 isolated from a serum collected in 1976: nucleotide sequence comparison to recent isolates and generation of hybrid HIV."				
RT	AIDS Res. Hum. Retroviruses 5:121-129(1989).				
RL					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	EMBL; M15896; AAB53948.1; -.				
DR	PIR; A44963; A44963.				
DR	HIV; M15896; ENV58321.				
DR	InterPro; IPR000328; Env_GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120.1.				
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.				
KW	SIGNAL.				
FT	CHAIN	1	29		
FT	CHAIN	30	511		
FT	CHAIN	512	856		
FT	DISULFID	53	73		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	118	206		TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	125	197		BY SIMILARITY.
FT	DISULFID	130	153		BY SIMILARITY.
FT	DISULFID	219	248		BY SIMILARITY.
FT	DISULFID	229	240		BY SIMILARITY.
FT	DISULFID	297	331		BY SIMILARITY.
FT	DISULFID	379	445		BY SIMILARITY.
FT	DISULFID	386	418		BY SIMILARITY.
FT	CARBOHYD	87	87		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	132	132		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	138	138		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	152	152		N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96909 MW; 839683F8BBBD174E CRC64;

Query Match 9.5%; Score 96.5; DB 1; Length 856;
Best Local Similarity 24.9%; Pred. No. 1.1; Indels 57; Gaps 10;

Matches 49; Conservative 20; Mismatches 71; Indels 57; Gaps 10;
QY 7 THLCPTVPNPASSI--ATWGGDFPKDKLNLKESDSDVNTEDRLKPC--STP----- 56
DB 70 THACVFPDPNPQELSLGNTVEKEFKDMKNVNEQHEHEDVISLMDQSLKPCVKLPLCYTILS 129
QY 57 SDKLIVDKLVNNGVNLQF-----IFDDEARTGQF-----NNLGEK 93
DB 130 CHNITTKDNNTVNTDEKEEIKNCSSYMTLELDKOKIYSLFYRLDIPVIGNSSNGDS 189
QY 94 NGY--VTC--PPRPDPLGKSFELVSPPEIPRKSQYLRSNMP----- 134
DB 190 SKRLRLNCNTSALTQACP-KVSEFPPIPIH-YCAPAGAILKCDDEDEGKPCPNANSTVQ 247
QY 135 ---GTRPEAKEQLIFSG 148
DB 248 CTGIGIRPVSTQLLLNG 264

RESULT 2
ID IL6B RAT STANDARD; PRT; 918 AA.
AC PA0190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor beta chain precursor (IL-6R-beta) (interleukin
6 signal transducer) (Membrane glycoprotein 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver.
RX MEDLINE=93052397; Pubmed=1427893;
RA Wang Y.; Nesbitt J.E.; Fuentes N.L.; Fuller G.M.;
RT Molecular cloning and characterization of the rat liver IL-6 signal
transducing molecule, gp130.";
RL Genomics 14:666-672(1992).
CC -!- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GP130 FOR INITIATING
SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC, RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,

CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 5 fibronectin type III domains.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
CC EMBL; M92340; -; NOT_ANNOTATED_CDS.
CC PIR; A44257; A44257.
CC HSSP; PA0189; 1BOU.
CC InterPro; IPR002986; CR1A.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003529; Hemopoietin_L_F2.
CC Pfam; PF00041; fn3; 3.
CC SMART; SMO0060; FN3; 4.
CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
CC Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
CC Repeat.
CC FT SIGNAL 1 22
CC FT CHAIN 23 918
CC FT DOMAIN 23 618
CC FT TRANSMEM 619 640
CC FT DOMAIN 641 918
CC FT DOMAIN 124 120
CC FT DOMAIN 124 221
CC FT DOMAIN 222 333
CC FT DOMAIN 324 422
CC FT DOMAIN 423 516
CC FT DOMAIN 517 754
CC FT DOMAIN 724 754
CC FT DISULFID 28 54
CC FT DISULFID 48 103
CC FT DISULFID 134 144
CC FT DISULFID 172 181
CC FT DISULFID 457 465
CC FT CARBOHYD 43 43
CC FT CARBOHYD 61 61
CC FT CARBOHYD 83 83
CC FT CARBOHYD 131 131
CC FT CARBOHYD 157 157
CC FT CARBOHYD 205 205
CC FT CARBOHYD 226 226
CC FT CARBOHYD 382 382
CC FT CARBOHYD 389 389
CC FT CARBOHYD 477 477
CC FT CARBOHYD 552 552
SQ SEQUENCE 918 AA; 102450 MW; 9818B6FEF087F7 CRC64;

Query Match 9.1%; Score 93; DB 1; Length 918;
Best Local Similarity 22.7%; Pred. No. 2.5;
Matches 58; Conservative 28; Mismatches 72; Indels 98; Gaps 14;

QY 11 WPTVPNPASSIATW-----HGDFDKL--NLKESDSD--VNTEDRLKPCSTPDKL 60
DB 651 WPNVDPSPSSHIAQWSPHTPRHNFNNSKQDMQSDANFTDVSVEIEANNNKPC--PDDLK 708
QY 61 VIDKLIVNNGVNLQRIFTDE--ARTGOENNIGG-----EKN----- 94
DB 709 SLD-----LFKKEKISTGHSGIGSSCMSSSRPSSISENEBNAOSTASTV 756
QY 95 ---GYVTCFPRDPCPLGKSF-----EELP-----VSEPEIPRKSQYL 129

Db 757 QSTVSHSGYRHOVSVQFSRSESTOPLDSEEREDDQLVDSDVSGDELLPQQOYFKQ 816
 QY 130 SRNPECTRPE-----AKEQLLFSGQSLVPHDLCEEGAPNPKNSVTARF- 175
 Db 817 SCGQCPASPDVSHFGSSQVPSGSEEDFRLKQOQVSDHSE-----P/-GSEQRRLQ 869
 QY 176 --LVSEKLPBHTKGEV 189
 Db 870 EGSVADALGTGTGQI 885

RESULT 3
 HXB9_HUMAN
 ID HXB9_HUMAN STANDARD; PRT; 250 AA.
 AC P17482; O9H111;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Homeobox protein Hox-B9 (Hox-2E) (Hox-2.5).
 GN HOXB9 OR HOX2E.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kosaki K., Kosaki R., Suzuki T., Yoshihashi H., Sasaki K., Matsuo N.;
 RT "A complete mutation analysis panel of human HOX genes."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdn T.B., Toshiyuki S., Carninci P., Prange S.J.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 173-250 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=89378558; PubMed=2570724;
 RA Giampao A., Acampora D., Zappalà V., Pannese M.,
 RA D'Esposito M., Care A., Faiella A., Scornaiuolo A., Russo G.,
 RA Simeone A., Boncinelli E., Peschle C.;
 RT "Differential expression of human HOX-2 genes along the anterior-
 posterior axis in embryonic central nervous system";
 RL Differentiation 40:191-197(1989).
 RN [4]
 RP SEQUENCE OF 185-250 FROM N.A.
 RX MEDLINE=90215256; PubMed=2576652;
 RA Boncinelli E., Acampora D., Pannese M., D'Esposito M., Somma R.,
 RA Gaudio G., Scornaiuolo A., Cafiero M., Faiella A., Simeone A.;
 RT "Organization of human class I homeobox genes";
 RL Genome 31:745-756(1989).
 CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
 A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
 SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.

CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE EMBRYOS AND FETUSES AT
 CC 5-9 WEEKS FROM CONCEPTION.
 CC -!- SIMILARITY: BELONGS TO THE ABD-B HOMEBOX FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AY014296; AAG42144.1; -
 CC EMBL; AY014295; AAG42144.1; JOINED.
 CC EMBL; BC015565; AAH15565.1; -
 CC EMBL; X16172; CA342294.1; -
 CC FIR; A37042; A37042.
 CC HSSP; P02833; 9ANT.
 CC TRANSFAC; T01738; -
 CC Genew; HGNC:5120; HOXB9.
 CC MIM; 142964; -
 CC GO; GO:0005634; C:nucleus; NAS.
 CC GO; GO:0003700; F:transcription factor activity; NAS.
 CC GO; GO:0007275; P:development; NAS.
 CC GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 CC InterPro; IPR001356; Homeobox.
 CC InterPro; IPR000047; HTH_lambdarepressor.
 CC Pfam; PF00046; homeobox_1.
 CC Pfam; PF04617; Hox9_act; 1.
 CC PRINTS; PR00024; HOMEBOX.
 CC PRINTS; PR00031; HTHREPRESSR.
 CC Prodom; PD00010; Homeobox; 1.
 CC SMART; SM00389; HOX; 1.
 CC PROSITE; PS00027; HOMEBOX_1; 1.
 CC PROSITE; PS00711; HOMEBOX_2; 1.
 CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
 CC Transcription regulation.
 CC FT DNA BIND 185 244 HOMEBOX.
 CC FT CONFLICT 173 173 T -> A (IN REF. 3).
 CC SEQ SEQUENCE 250 AA; 28058 MW; F06ECB08BBD2C CRC64;

Query Match 9.0%; Score 92; DB 1; Length 250;
 Best Local Similarity 21.6%; Pred. No. 0.6;
 Matches 38; Conservative 27; Mismatches 57; Indels 54; Gaps 8;

QY 40 DSVNTEPRILKPCSTPSDKLYIDKLVDVFNFGVLTQETTDARTGQENNLGGEKNGYTC 99
 Db 13 DSIHSEEDAPPAKPSGQ-----YASSRQPSHAHL-----EPSC 50
 QY 100 PRPDCPL-GKSFELPVSP-----IPPKSQYLSRMEPTGRPEAK 141
 Db 51 SPQPAVPFGASW--APLSFHASGSLPSVTHPIYIOPQVPPAESRYLTWLEPPARGENA 108
 QY 142 EQLLFSGQSLV-----PDHLCGEGAPNPKNSVTARELVSEKLPBHTKGEV 189
 Db 109 PG--QGQAAYVAEPFLGAPGLKGTPEVSLETS-AGREAVLSNQPGVDNNT 160

RESULT 4
 ENV_HVLEL
 ID ENV_HVLEL STANDARD; PRT; 853 AA.
 AC P04581;
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11689;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=86245056; Pubmed=2424612;
RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
CC -----
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CC -----
DR EMBL; K03454; AAA44329.1; -;
DR EMBL; A07108; CAA00616.1; -;
DR HIV; K03454; ENV\$SELT.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 53 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 87 416 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96721 MW; F9CDB64DAAD07A5 CRC64;
Query Match 8.9%; Score 90.5; DB 1; Length 853;
Best Local Similarity 22.3%; Pred. No. 3.8;
Matches 49; Conservative 21; Mismatches 63; Indels 87; Gaps 10;

QY 7 THLCPTVPNPAESSI--ATWHDGDFKOKLNLKESDSDVNTEDRLIKPCSTPSDKLVYDK 64
Db 70 THACVPTDNPQELALENTVENFNMKNMVMQWMDIISLWDQSLKFC-----VKLTP 123
QY 65 LVVNGVNVQELFTDEARG--QENNNGEKKKGYVTCPP-----RPD 104
Db 124 LCVTLN-----CSBLRNNGTMGNVTEEGMKNCGFNVTVLKKKKQVVALPYRLD 177
QY 105 -----CPLKSFEEELPVSPDIPPRKSQYLRSR----- 131
Db 178 IYVINDSTNSTNRLINCNTSALTQACP-KVSTFEPIDH-YCAPAGRAILKCKDKKN 235
QY 132 -----MPGTPPEAKEQLLFGQSIVPDLCEE 159
Db 236 GTGPCTNVSTVQCTHGIRPVSTQLLNGS-----LAEE 269
RESULT 5
ENV_HVJ3 STANDARD; PRT; 867 AA.
ID ENV_HVJ3
AC P12489;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-OUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120), Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
OS viruses; Retrod virus; Retroviridae; Lentivirus.
OX NCBI_Taxid=11694;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=869352108; Pubmed=2669897;
RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria."
RL Aids Res. Hum. Retroviruses 5:411-419(1989).
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CC -----
DR EMBL; M21138; AA03526.1; -;
DR HIV; M21138; ENV\$3H3.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 457 BY SIMILARITY.
FT DISULFID 395 450 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 867 AA; 98399 MW; 5F23101468B8E860 CRC64;

Query Match 8.9%; Score 90.5; DB 1; Length 867;
 Best Local Similarity 22.7%; Pred. No. 3.9;
 Matches 46; Conservative 28; Mismatches 60; Indels 69; Gaps 10;

QY 7 TLHCFTVPNPAESSIATWHDGDFKDKLNKES-----DSSVNTEDRIKPC-STPS 57
 DB 70 THACVPTDPNPEVVL-----ENVTKEFNMKNMVEQMHEDTISLMDOSLKCVKLTLP- 123
 QY 58 DKLVIDKLVNFEVNGEIFTDEARTGOENNLGE-KNGVYVTPFPDPCLGKSFELRY 116
 DB 124 --LCVTLCIDWGNDSNPATNTTSGGEMKEGEMKN-----CSF----- 162
 QY 117 SPEIPRKSQYLRSMEPTGRPEAKCOLFSGSLVDHLCBEGAPNYLKNSTAREFL 176
 DB 163 -----NITTSIDKY-----QKHALFYKRDVVPIN-----NSTKONIKNDNSTRYL 205
 QY 177 VS-----EKLPEH 184
 DB 206 ISCNTSVITQACPISFEPIPIH 228

RESULT 6
 ENV_HVIND STANDARD; PRT; 846 AA.
 AC P18799;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11695;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90034200; PubMed=2806917;
 RA Spire B., Sire J., Zacher V., Rey F., Barre-Sinoussi F., Galibert F.,
 RA Hampe A., Chermann J.C.;
 RT "Nucleotide sequence of HIV-1 NDK: a highly cytopathic strain of the
 RT human immunodeficiency virus.";
 RL Gene 81:275-284(1989).
 CC -1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH
 CC AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.

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CC EMBL; M27323; AAA4873.1; -;
 CC PIR; J00066; VCLJND.
 CC HIV; M27323; ENV\$NDK.
 CC InterPro; IPR000328; Env GP41.
 CC InterPro; IPR000777; GP120.
 CC Pfam; PF00516; GP120; 1.
 CC Pfam; PF00517; GP41; 1.
 CC Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 CC Signal.
 KW SIGNAL.
 FT CHAIN 1 29
 FT DISULFID 30 501
 FT DISULFID 52 846
 FT DISULFID 53 73
 FT DISULFID 118 200
 FT DISULFID 125 191
 FT DISULFID 130 152
 FT DISULFID 213 242
 FT DISULFID 223 234
 FT DISULFID 291 328
 FT DISULFID 374 435
 FT DISULFID 381 408
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 151 151
 FT CARBOHYD 179 179
 FT CARBOHYD 182 182
 FT CARBOHYD 229 229
 FT CARBOHYD 236 236
 FT CARBOHYD 257 257
 FT CARBOHYD 271 271
 FT CARBOHYD 284 284
 FT CARBOHYD 290 290
 FT CARBOHYD 351 351
 FT CARBOHYD 382 382
 FT CARBOHYD 388 388
 FT CARBOHYD 392 392
 FT CARBOHYD 395 395
 FT CARBOHYD 401 401
 FT CARBOHYD 438 438
 FT CARBOHYD 451 451
 FT CARBOHYD 452 452
 FT CARBOHYD 601 601
 FT CARBOHYD 606 606
 FT CARBOHYD 615 615
 FT CARBOHYD 627 627
 SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DA527DE2E83 CRC64;

Query Match 8.5%; Score 86; DB 1; Length 846;
 Best Local Similarity 20.2%; Pred. No. 9.2;
 Matches 49; Conservative 23; Mismatches 74; Indels 96; Gaps 9;

QY 7 TLHCFTVPNPAESSI-ATWHDGDFKDKLNKESDSSVNTEDRIKPCSTSDKLVIDK 64
 DB 70 THACVPTDPNPEVLENTENFNMKNMVEQMHEDTISLMDOSLKPC-----VKLTP 123
 QY 65 LVVNFENVLQEIFTDARTGOENNLGEGKNGVYVTPFR----- 102
 DB 124 LCVTLN-----CTBELRNSKNGKNGVBEERKKNKSFNVRDGRBOVYALFYLDIVPIDN 177
 QY 103 -----PDCPIKSFSEELIPVSEELIPRKSQYLRSS----- 131
 DB 178 NNRRTSTNYRLINCSTSTTQACP-KISFEPIPIH-FCAPAFALIKCKDKKFGNGTPCS 235
 QY 132 -----MPGSTRPEAKCOLFSGSLVDPHLCBEGAPNYLKNSTAREFLV-SEKLPEH 184
 DB 236 NVSTWQCTHGIRPVVSTOLLNG-----SLAEBEITIRSESLTN 275
 QY 185 TK 186

FT SITE 760 760 IN-FRAME TERMINATION CODON.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 160 BY SIMILARITY.
 FT DISULFID 219 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.
 FT DISULFID 296 330 BY SIMILARITY.
 FT DISULFID 376 439 BY SIMILARITY.
 FT DISULFID 383 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600BA7A08 CRC64;

Query Match 8.5%; Score 86; DB 1; Length 856;
 Best Local Similarity 29.6%; Pred. No. 9.3;
 Matches 23; Conservative 19; Mismatches 42; Indels 8; Gaps 4;
 QY 7 THLCWPTVPNPAESSI--ATWGDGDFKDKLNLKESDVSNTEDRIILKPCSTPSDKLVIDK 64
 DB 70 THACVPTDPRQGVVIGVNTENMMNNVQGMHEDIISLMDQSLKPCV---KLTPLC 125
 QY 65 LVVNFQVNLQEIITDEARTGQENNIGGEKNGVYT-CPF 101
 DB 126 VTLNCTNLNRDSTINATNT-TSSNRGMEGEGENTNCSF 162

RESULT 9
 TGT_CLOPE
 ID TGT_CLOPE STANDARD; PRT; 380 AA.
 AC 08XJ16;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE transglycosylase (EC 2.4.2.29) (tRNA-guanine
 transferase)
 GN TGT OR CPE1945.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN 1;
 RP SEQUENCE FROM N.A.

RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohsuima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
 CC -1- FUNCTION: Exchanges the guanine residue with 7-aminomethyl-7-
 deazaguanine in tRNAs with GU(N) anticodons (tRNA-Asp, -Asn, -His
 and -Tyr). After this exchange, a cyclopentimidic moiety is
 attached to the 7-aminomethyl group of 7-deazaguanine, resulting
 in the hypermodified nucleoside quenosine (Q) (7-((4,5-cis-
 dihydroxy-2-cyclopenten-1-yl)amino)methyl)-7-deazaguanosine (By
 similarity).
 CC -1- CATALYTIC ACTIVITY: tRNA guanine + guanine = tRNA guanine +
 guanine.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE QUEUINE tRNA-RIBOSYLTRANSFERASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC CC
 CC EMBL, AP001197; BAB81651.1; -.
 DR HAMAP, MF_00168; -; 1.
 DR InterPro, IPR004803; QtrRNA_ribo_trans.
 DR InterPro, IPR002616; tRNA_ribo_trans.
 DR Pfam, PF01702; TGT, 1.
 DR TIGRPFAMs, TIGR00430; Q tRNA tgt; 1.
 DR TIGRPFAMs, TIGR00449; tgt_general; 1.
 KW Quenosine biosynthesis; Transferase; Glycosyltransferase;
 KW tRNA processing; Zinc; Complete proteome.
 FT ACT SITE 94 94 BY SIMILARITY.
 FT METAL 276 276 ZINC (BY SIMILARITY).
 FT METAL 313 313 ZINC (BY SIMILARITY).
 FT METAL 315 315 ZINC (BY SIMILARITY).
 FT METAL 318 318 ZINC (BY SIMILARITY).
 FT METAL 344 344 ZINC (BY SIMILARITY).
 SQ SEQUENCE 380 AA; 43200 MW; B0B7C41D254BED8 CRC64;

Query Match 8.4%; Score 85; DB 1; Length 380;
 Best Local Similarity 25.8%; Pred. No. 4.1;
 Matches 33; Conservative 19; Mismatches 40; Indels 36; Gaps 5;
 QY 14 VNPA-----ESSIA---TWGDDPFKDKLNLKESDVSNTEDRIILKPCSTPSDKLVIDK 65
 DB 150 INPSTREVESVARTTRMLERCKKEMDRNLSDTNNKQMLG----- 195
 QY 66 VVNFQVNLQEIITDEARTGQENNIGGEKNGVYT-CPFPDCKPKGSPBEL-----PVSPET 120
 DB 196 -INQGGVYEDIRIEHAKTIREMDLDGYAIGLA-----VGETHEMYRYIDAVVPHL 246
 QY 121 PPKSGYL 128
 DB 247 PEDKPYL 254

RESULT 10
 PRD1_MOUSE
 ID PRD1_MOUSE STANDARD; PRT; 856 AA.
 AC 060636;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-FEB-2003 (Rel. 42, Last annotation update)
 DE PR-domain zinc finger protein 1 (beta-interferon gene positive-
 regulatory domain 1 binding factor) (BLIMP-1).
 GN PRDM1 OR BLIMP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RX MEDLINE=94221646; PubMed=8168136;
RA Turner C.A., Mack D.H., Davis M.M.;
RT "Blimp-1, a novel zinc finger-containing protein that can drive the
RT maturation of B lymphocytes into immunoglobulin-secreting cells.",
RL Cell 77:297-306(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=20572522; PubMed=11121475;
RA Tunayapin C., Shapiro M.A., Calame K.L.;
RT "Characterization of the B lymphocyte-induced maturation protein-1
RT (blimp-1) gene, mRNA isoforms and basal promoter.";
RL Nucleic Acids Res. 28:4846-4851(2000).
CC -1- FUNCTION: Transcriptional repressor that binds specifically to the
CC PRD1 element in the promoter of the beta-interferon gene. Drives
CC the maturation of B lymphocytes into Ig secreting cells.
CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC -1- SIMILARITY: Contains 1 SET domain.
CC -----
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CC -----
DR EMBL; U08185; AAA19252.1; -
DR EMBL; AF305539; AAC42212.1; -
DR EMBL; AF305534; AAC42212.1; JOINED.
DR EMBL; AF305535; AAC42212.1; JOINED.
DR EMBL; AF305536; AAC42212.1; JOINED.
DR EMBL; AF305537; AAC42212.1; JOINED.
DR EMBL; AF305538; AAC42212.1; JOINED.
DR PIR; A51503; A51503.
DR HSSP; P08048; 72NF.
DR TRANSFAC; T02316; -
DR MGD; MGI:96655; Ptdml.
DR InterPro; IPR001214; SET.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF008856; SET; 1.
DR Pfam; PF008856; Zf_C2H2; 5.
DR ProDom; PD000003; Znf_C2H2; 1.
DR SMART; SM00317; SET; 1.
DR SMART; SM00355; Znf_C2H2; 4.
DR PROSITE; PS00280; SET; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 4.
KW Transcription regulation; Repressor; DNA-binding; Zinc-finger;
KW Metal-binding; Nuclear protein; Repeat.
FT DOMAIN 118 237 SET.
FT ZN_FING 606 628 C2H2-TYPE.
FT ZN_FING 634 656 C2H2-TYPE.
FT ZN_FING 662 684 C2H2-TYPE.
FT ZN_FING 690 712 C2H2-TYPE.
SQ SEQUENCE 856 AA; 95835 MW; B9AC6FC2E29ECFAA CRC64;
Query Match 8.3%; Score 84; DB 1; Length 856;
Best Local Similarity 22.1%; Pred. No. 14;
Matches 43; Conservative 33; Mismatches 81; Indels 38; Gaps 9;
QY 15 PNPASSIATWHDGDFKDKL-----NKKESDPS---VNTEDRIKPCSTPSDKL 60
DB 221 PIRANGELIWMYCRDFAERLHYPPGSLVITNLQTESNKQYSSSEGNELYPSSVKKREY 280
QY 61 VIDKLIVNFGN--VLQEIFTDEAR--TGQENNIKGEKNGVYTCPPRP-----DCLPKGS 110
DB 281 SVKEILLIDSNPSKRDIVRSNISPTLEKMDGFRKNGSPDMFPYRVVYPIRALPLED 340

QY 111 FEELVPSPEIPPRKSOYL-RSRMPEGTPEAKEQLFSGQSLVDPHLCBEGAPNPLYKNS 169
DB 341 F--LKASLAVGMERPTVITHSPISSTSPSP-----ASSSPQSLKSSSPHSPGNT 391
QY 170 VTAREFLVSEKLPKH 184
DB 392 VSP---LAPGLPEH 402
RESULT 11
ID COAT_PAVH STANDARD; PRT; 722 AA.
AC P03136;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coat protein VP1 (Contains: Coat protein VP2).
OS Hamster parovirus H1.
OS Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10799;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83112183; PubMed=6823009;
RA Rhode S.L. III, Paradiso P.R.;
RT "Parovirus genome: nucleotide sequence of H-1 and mapping of its
RT genes by hybrid-arrested translation.";
RL J. Virol. 45:173-184(1983).
CC -1- SIMILARITY: BELONGS TO THE PARVOVIRUSES COAT PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X01457; CAB57285.1; ALT_SEQ.
DR PIR; A03699; VCPV12.
DR HSSP; P07302; 1MW1.
DR InterPro; IPR001403; Parvo_coat.
DR Pfam; PF00740; Parvo_coat; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 722
FT CARBOHYD 178 722 COAT PROTEIN VP1.
FT CARBOHYD 218 722 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 647 647 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 675 675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN 155 170 GLY-RICH
SQ SEQUENCE 722 AA; 79737 MW; 6BB678391A5DC31 CRC64;
Query Match 8.2%; Score 83.5; DB 1; Length 722;
Best Local Similarity 20.8%; Pred. No. 12;
Matches 43; Conservative 25; Mismatches 82; Indels 57; Gaps 8;
QY 4 NKTLHCWPTVNPABSSI---ATWHDGDFKDKLNLKESDPSVNTEDRIKPCSTPSDKL 54
DB 197 SRLHLHGMPSESNYKRVVTHNNQTTGHGTVKXGNN-----AYDTHQOIWTPWISLVVAN 249
QY 55 -----TPSDKVIDKLV--VNFQVLDIEFTDEARTQENNLGGE-----KNGVYTC 99
DB 250 ANGWFQPSDWDQFIONSMESLWLSLSELFVNVVKTVTBQGAQDALKYNNNDLTACM 309
QY 100 -----PRPDCPLKSPFEELPVSEIIP-----PRKSOYLRSRMPEGTR--- 137
DB 310 MWALDSNNILPYTPAAQISSETIGFYPWKPTAPAPRYFFPMWRQSLSVYSSNABEGQITD 369
QY 138 ---PRAEQQLIFSGQSLVDPHLCBEG 160
DB 370 TIGEPQALNSQFTTENTLPIILRLTG 396

DR SMART; SM00259; ZnF_A20; 7.
DR PROSITE; PS50802; OTU; 1.
KM Apoptosis; DNA-binding; Zinc-finger; Repeat.
FT DOMAIN 92 263 OTU
FT REPEAT 286 356 2 X APPROXIMATE REPEATS.
FT REPEAT 286 317 1.
FT DOMAIN 324 356 2.
FT DOMAIN 369 775 INTERACTION WITH NAF1 (BY SIMILARITY).
FT DOMAIN 387 782 ZINC-FINGERS.
FT ZN_FING 387 407
FT ZN_FING 478 498
FT ZN_FING 521 539
FT ZN_FING 607 627
FT ZN_FING 657 677
FT ZN_FING 716 736
FT ZN_FING 762 782
SO SEQUENCE 790 AA; 89613 MW; 320AEA97F5BD4491 CRC64;

Query Match 8.1%; Score 82.5; DB 1; Length 790;
Best Local Similarity 25.6%; Pred. No. 17;
Matches 33; Conservative 17; Mismatches 48; Indels 31; Gaps 5;

QY 75 EIFTDEARTGQENNLGGEKNGVTCPPR-----PDCLGKSFELVSPR 119
DB 347 ELVQHEKXKQKQSEQRRRGGHQNPEPSVPLSLMDVKCTETPCPFNFVNTQPLCHE 406
QY 120 IPRKSO-----YLRSRM-PEG-----TRPEAKRQLFS-GOSLVDPDLCEGAPY 163
DB 407 CSRRQKQKMLKLNKSKPPEGLPGMALGASGAEVPLANNPESTGGPHAPPTAAS 466
QY 164 PYLKNVTA 172
DB 467 PFLFSETTA 475

RESULT 14
ENV_HVLMF STANDARD; PRT; 853 AA.
AC P19551;
ID ENV_HVLMF STANDARD; PRT; 853 AA.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C.,
RA Maslak A.;
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis."
RL J. Virol. 64:3792-3803 (1990).
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CC -----
CC EMBL; M33943; AAA44850.1; -.
DR PDB; 1A1K; 16-JUN-97.
DR HIV; M33943; ENVSMFA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.

KM AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
KM 3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 31 509 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74
FT DISULFID 119 203 BY SIMILARITY.
FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 8.1%; Score 82.5; DB 1; Length 853;
Best Local Similarity 22.7%; Pred. No. 19;
Matches 49; Conservative 18; Mismatches 66; Indels 83; Gaps 10;

QY 7 THLCPTVNPAPASSI--ATWGGDFKDLNKLKESDSDSVNEDRLILKPCSTPSDKLVLDK 64
DB 71 THACVPTDNPPEVILVNTENFDMWMDVQGMHEDILSLMDQSLKNC-----VKLTP 124
QY 65 LVVFNQNVLOEITFTDEARTGQENNLG--EKNGVTCPP----- 101
DB 125 LCVNKK-----CTDLKNDNTNNSNGRMIMKEGIRKCSFNISIRNKQKEYAFYK 178
QY 102 ---RP-----DCLGKSFELVSPRIPRKSOYLRS----- 130
DB 179 LDIRPIDNTTYRLISCMNTSVITQACP-KVSFFPIPIH-YCAPAGRAILKCNKDTNGTGP 236
QY 131 -----RMPESTRPEAKRQLFSGOSLVDPDLCEH 159
DB 237 CINVSTVQCTHGRIRPVVSQILLNS-----LAE 266

RESULT 15
ENV_HVLMF STANDARD; PRT; 861 AA.
AC P31819;
ID ENV_HVLMF STANDARD; PRT; 861 AA.
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:47 ; Search time 66.8907 Seconds
(without alignments)
729.128 Million cell updates/sec

Title: US-09-892-949-2_COPY_544_732

Perfect score: 1017
Sequence: 1 KKPNKLTLCWPTVNPAPES.....VTAREFLVSEKLPHTKGGEV 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp Unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	100.0	732	Q8N117	Q8N117 homo sapien
2	483.5	47.5	716	Q8K5B1	Q8K5B1 mus musculu
3	479.5	47.1	235	Q8BSU3	Q8BSU3 mus musculu
4	479.5	47.1	716	Q8R501	Q8R501 mus musculu
5	115	11.3	801	Q99BY7	Q99BY7 human immun
6	115	11.3	801	Q99BX7	Q99BX7 human immun
7	104.5	10.3	503	Q74827	Q74827 human immun
8	104	10.2	501	Q75951	Q75951 human immun
9	104	10.2	501	Q75939	Q75939 human immun
10	103	10.1	501	Q75937	Q75937 human immun
11	103	10.1	501	Q75942	Q75942 human immun
12	102.5	10.1	791	Q99BX1	Q99BX1 human immun
13	100	9.8	515	Q74304	Q74304 human immun
14	99.5	9.8	865	Q9QGM8	Q9QGM8 human immun
15	99	9.7	800	Q99BY1	Q99BY1 human immun
16	98.5	9.7	869	Q91V33	Q91V33 human immun

17	98	9.6	795	15	Q99BX6	Q99BX6 human immun
18	98	9.6	864	15	Q9E610	Q9E610 simian-huma
19	98	9.6	871	15	P88155	P88155 human immun
20	97.5	9.6	788	15	Q99BY6	Q99BY6 human immun
21	97	9.5	855	15	Q75837	Q75837 human immun
22	97	9.5	856	15	Q9DS18	Q9DS18 human immun
23	97	9.5	860	15	Q9E1S6	Q9E1S6 human immun
24	96.5	9.5	855	15	Q9YKQ4	Q9YKQ4 human immun
25	96.5	9.5	856	15	Q9Q2G3	Q9Q2G3 human immun
26	96	9.4	475	15	Q9WR11	Q9WR11 human immun
27	95.5	9.4	854	15	Q9QMH2	Q9QMH2 human immun
28	95.5	9.4	855	15	Q9QD15	Q9QD15 human immun
29	95.5	9.4	857	15	Q9Q0Q6	Q9Q0Q6 human immun
30	95	9.3	479	15	Q76124	Q76124 human immun
31	95	9.3	805	15	Q99BY5	Q99BY5 human immun
32	95	9.3	849	15	Q41803	Q41803 human immun
33	95	9.3	859	15	P87924	P87924 human immun
34	95	9.3	1281	11	Q9R1P5	Q9R1P5 mus musculu
35	94.5	9.3	756	15	Q99BW9	Q99BW9 human immun
36	94.5	9.3	848	15	Q69988	Q69988 human immun
37	94.5	9.3	848	15	Q69990	Q69990 human immun
38	94.5	9.3	856	15	Q72993	Q72993 human immun
39	94.5	9.3	858	15	Q75114	Q75114 human immun
40	94	9.2	482	15	Q9WR14	Q9WR14 human immun
41	94	9.2	794	15	Q99BY3	Q99BY3 human immun
42	94	9.2	856	15	P90115	P90115 human immun
43	94	9.2	862	15	Q9WLG8	Q9WLG8 human immun
44	94	9.2	863	15	Q9Q6H1	Q9Q6H1 human immun
45	93.5	9.2	529	15	Q77979	Q77979 human immun

ALIGNMENTS

RESULT 1

Q8N117 PRELIMINARY; PRT; 732 AA.
ID Q8N117
AC Q8N117;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Gp130-like monocycle receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21988187; PubMed=11877449;
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals Proliferation, and Activates STAT-3 and STAT-5.";
RL J. Biol. Chem. 277:16831-16836(2002).
DR EMBL; AF486620; AAM27958.1; -
DR InterPro; IPR002396; CRIA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 3.
DR Receptor.
SQ SEQUENCE 732 AA; 82953 MW; 30F84BD3DD9A20E CRC64;

Query Match 100.0%; Score 1017; DB 4; Length 732;

Best Local Similarity 100.0%; Pred. No. 6,2e+89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	KKPNKLTLCWPTVNPAPESIAIWHGDPKDKLNLKESDSDSVNTEDEILKPCSTPSDKL	60
DB	544	KKPNKLTLCWPTVNPAPESIAIWHGDPKDKLNLKESDSDSVNTEDEILKPCSTPSDKL	603
QY	61	VIDKLVNFGNVLQELIFDEARTGEENLIGEKNGYVTCPPRPDCLPKSFELVSPDI	120
DB	604	VIDKLVNFGNVLQELIFDEARTGEENLIGEKNGYVTCPPRPDCLPKSFELVSPDI	663

QY 121 PPRKSOYLRSRMPEGTREPEAKQQLPFGQSLVDPDHLCEEGAPNPYLKNSVTAREPLVSEK 180
DB 664 PPRKSOYLRSRMPEGTREPEAKQQLPFGQSLVDPDHLCEEGAPNPYLKNSVTAREPLVSEK 723
QY 181 LPEHTKGEV 189
DB 724 LPEHTKGEV 732

RESULT 2

Q8K5B1 PRELIMINARY; PRT; 716 AA.

AC Q8K5B1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Gp130-like monocyte receptor.
GN GLMR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=2198187; PubMed=11877449;
RA Chillard N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals
RT Proliferation, and Activates STAT-3 and STAT-5.";
RL J. Biol. Chem. 277:16831-16836(2002).
DR EMBL; AF486621; AA027959.1; -
DR MGD; MGI:2180511; GIMR.
DR InterPro; IPR002996; CR1A.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 3.
KW Receptor.
SQ SEQUENCE. 716 AA; 80641 MW; 3986B0B253F7C7E5 CRC64;

Query Match 47.1%; Score 483.5; DB 11; Length 716;
Best Local Similarity 56.0%; Pred. No. 9,7e-38;
Matches 107; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 1 KKPENKLTLCWPTVNPAPASSIATWQDDFKDKLNLKESDVSNTEDRLKPCSTPSDKL 60
DB 531 RKENRLTLPCCPDVNPAPASSIATWLGDFK-KSNMKETGNSGNTEDVTLKPCVPAD-- 587
QY 61 VIDKLVPNGVNLQEIFTDARTQGENNLGEGKNGVYTCPPRPDCPLGKSFELVSPRI 120
DB 588 LIDKLVPNFENLEVLVTEBAGKQASILGEGANEVYTSRDPDPGKSFKEPSILTEV 647
QY 121 PPRKSOYLRSRMPEGTREPEAKQQLPFGQSLVDPDHLCEEGAPNPYLKNSVTAREPLV 178
DB 648 ASDSHSTCSRMDAYSELARQPSSCQSPGLSPPR--EDQANPYLKNSTTREFLVH 705
QY 179 EKLPEHTKGEV 189
DB 706 ENPEHSKGEV 716

RESULT 3

Q8BSU3 PRELIMINARY; PRT; 235 AA.

AC Q8BSU3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=pituitary;
RX MEDLINE=22354683; PubMed=1246851;
RA The FANTOM Consortium,
RA the Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030512; BAC26998.1; -
KW Hypothetical protein.
SQ SEQUENCE. 235 AA; 25133 MW; 50928397A1AD126F CRC64;

Query Match 47.1%; Score 479.5; DB 11; Length 235;
Best Local Similarity 56.0%; Pred. No. 5.7e-38;
Matches 107; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 1 KKPENKLTLCWPTVNPAPASSIATWQDDFKDKLNLKESDVSNTEDRLKPCSTPSDKL 60
DB 50 RKENRLTLPCCPDVNPAPASSIATWLGDFK-KSNMKETGNSGNTEDVTLKPCVPAD-- 106
QY 61 VIDKLVPNGVNLQEIFTDARTQGENNLGEGKNGVYTCPPRPDCPLGKSFELVSPRI 120
DB 107 LIDKLVPNFENLEVLVTEBAGKQASILGEGANEVYTSRDPDPGKSFKEPSILTEV 166
QY 121 PPRKSOYLRSRMPEGTREPEAKQQLPFGQSLVDPDHLCEEGAPNPYLKNSVTAREPLV 178
DB 167 ASDSHSTCSRMDAYSELARQPSSCQSPGLSPPR--EDQANPYLKNSTTREFLVH 224
QY 179 EKLPEHTKGEV 189
DB 225 ENPEHSKGEV 235

RESULT 4

Q8RS01 PRELIMINARY; PRT; 716 AA.

AC Q8RS01;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Cytokine receptor NR10.
GN GLMR OR NR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
RT "Polymorphism between C57BL/6 and Balb/c in the novel cytokine
RT receptor NR10.";
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083111; BAB86745.1; -
DR MGD; MGI:2180511; GIMR.
DR InterPro; IPR002996; CR1A.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 3.
KW Receptor.
SQ SEQUENCE. 716 AA; 80598 MW; CBF718DCCD40FC7 CRC64;

Query Match 47.1%; Score 479.5; DB 11; Length 716;
Best Local Similarity 56.0%; Pred. No. 2.3e-37;
Matches 107; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 1 KKPENKLTLCWPTVNPAPASSIATWQDDFKDKLNLKESDVSNTEDRLKPCSTPSDKL 60
DB 531 RKENRLTLPCCPDVNPAPASSIATWLGDFK-KSNMKETGNSGNTEDVTLKPCVPAD-- 587
QY 61 VIDKLVPNGVNLQEIFTDARTQGENNLGEGKNGVYTCPPRPDCPLGKSFELVSPRI 120
DB 588 LIDKLVPNFENLEVLVTEBAGKQASILGEGANEVYTSRDPDPGKSFKEPSILTEV 647

QY 121 PPRKQYLASRMPEGTRPEAKBQLFSGOS--LVPHLCBEGAPNPYLNSTAREFLVS 178
DB 648 ASSEDSHSTCSRMADSEYSEIARQPSSSCSQPSLSPR--EDQKQNPYLKNSVTTREFLVH 705
QY 179 EKLPEHTKGEV 189
DB 706 ENIPEHSGEV 716

RESULT 5

Q99BX7 PRELIMINARY; PRT; 801 AA.
AC Q99BX7; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
EN Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Suthent R., Srisurapanon S.;
RT "Biological and immunological characteristics of HIV-1 subtype E in
cerebrospinal fluid and blood."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF22195; AAK09402.1; -
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 801
FT SEQUENCE 801 AA; 90874 MW; 25FD34841FB1153 CRC64;

Query Match 11.3%; Score 115; DB 15; Length 801;
Best Local Similarity 24.0%; Pred. No. 0.026;
Matches 58; Conservative 30; Mismatches 78; Indels 76; Gaps 12;

QY 7 THLCWPTVNPAPSSSI--ATWGGDDFKDKLNKESDSDVNTEDRIKPC--STP----- 56
DB 18 THACVPTDPNPQEMPLKNTVENFNMMKNMAEQMEDVISLMDQSLKPCVKLTPLCVTLTD 77
QY 57 -----SDKLVIDKLVNFGVNLQEI-----FTDEARTGOE----- 86
DB 78 CTYANMTTANLITDSKNSIRII--GNLTBEVRNCSFNMTELRDRQKQVHTLFYKLDIV 134
QY 87 --NNLGEKNGVYTC--PRPDCPLGKSFEEPLVSPSEIP-----PRK 124
DB 135 PIDSNNHSHKYRLINCNSNVKQACP-KISFDPIPHYCTPAGYAILKCNKKFNGTGPK 193
QY 125 SQYLASRMPEGTRPEAKBQLFSGOSLVDPDHLCBEGAPNPYLNSTAREFLVSEKLP 184
DB 194 -DVSVVQCTHGKIPVSTQLVNGS-----LAEEING--KSSRRRIITISSENLTN 243
QY 185 TK 186
DB 244 AK 245

RESULT 6

Q99BX7 PRELIMINARY; PRT; 801 AA.
AC Q99BX7; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
EN Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Suthent R., Srisurapanon S.;
RT "Biological and immunological characteristics of HIV-1 subtype E in
cerebrospinal fluid and blood."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF22205; AAK09412.1; -
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 1 801
FT SEQUENCE 801 AA; 90833 MW; 04FA14142P6D37A4 CRC64;

Query Match 11.3%; Score 115; DB 15; Length 801;
Best Local Similarity 24.0%; Pred. No. 0.026;
Matches 58; Conservative 30; Mismatches 78; Indels 76; Gaps 12;

QY 7 THLCWPTVNPAPSSSI--ATWGGDDFKDKLNKESDSDVNTEDRIKPC--STP----- 56
DB 18 THACVPTDPNPQEMPLKNTVENFNMMKNMAEQMEDVISLMDQSLKPCVKLTPLCVTLTD 77
QY 57 -----SDKLVIDKLVNFGVNLQEI-----FTDEARTGOE----- 86
DB 78 CTYANMTTANLITDSKNSIRII--GNLTBEVRNCSFNMTELRDRQKQVHTLFYKLDIV 134
QY 87 --NNLGEKNGVYTC--PRPDCPLGKSFEEPLVSPSEIP-----PRK 124
DB 135 PIDSNNHSHKYRLINCNSNVKQACP-KISFDPIPHYCTPAGYAILKCNKKFNGTGPK 193
QY 125 SQYLASRMPEGTRPEAKBQLFSGOSLVDPDHLCBEGAPNPYLNSTAREFLVSEKLP 184
DB 194 -DVSVVQCTHGKIPVSTQLVNGS-----LAEEING--KSSRRRIITISSENLTN 243
QY 185 TK 186
DB 244 AK 245

RESULT 7

Q74827 PRELIMINARY; PRT; 503 AA.
AC Q74827; 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
EN Envelope glycoprotein gp120 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Blouin J.;
RT Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U43110; AAA85201.1; -
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
FT NON_TER 503
FT SEQUENCE 503 AA; 53F94F51217B1C4A CRC64;

Query Match 10.3%; Score 104.5; DB 15; Length 503;
Best Local Similarity 23.6%; Pred. No. 0.15;
Matches 43; Conservative 27; Mismatches 91; Indels 21; Gaps 6;

QY 7 THLCWPTVNPAPSSSI--ATWGGDDFKDKLNKESDSDVNTEDRIKPCSTSDKLVIDK 64
DB 70 THACVPTDPNPQEMPLKNTVENFNMMKNMAEQMEDVISLMDQSLKPCVKLTPLCVTLR 129

QY 65 LV-VNFGNVLOEIFTDEARTGOENNLGEGNGVYTCFPRDCLPKGSFEE-----113
 DB 130 CTANFTNATDAVATN--ATAKNATKEMNTYKNGSFNNTTSLGDKHQVSLFFYKDL 187
 QY 114 LVPSPFIPPKSQYLRSRMPEGTRPEAKEQLFSGGSLVPHLCESGAPNPYIKNSVTAR 173
 DB 188 VPIDGINDGNNSSEYIILHCTSVIKQACPKVSFDP--IPHYC---APADFAILKCNDK 241
 QY 174 EF 175
 DB 242 EF 243

RESULT 8

Q75951 PRELIMINARY; PRT; 501 AA.
 AC Q75951;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DB (Clone B1BR002W.01062aED) proviral 5' ORF (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brazil;
 RA Ranjbar S., Holmes H.;
 RT "Molecular Characterization of HIV-1 isolate from Brazil."
 RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L35493; AAA72447.1; -
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 501
 SQ SEQUENCE 501 AA; 56483 MW; 36291BA1BFED54CB CRC64;

Query Match 10.2%; Score 104; DB 15; Length 501;
 Best Local Similarity 25.3%; Pred. No. 0.16; 71; Indels 26; Gaps 8;
 Matches 41; Conservative 24; Mismatches 71; Indels 26; Gaps 8;
 QY 7 THLCWPTVPNPAESSI--ATWGGDDFKDKLNLKESDVSNTEDRIILKPCSTPDKLVYDK 64
 DB 71 THACVPTDPNPGQEVVLENTYENFMNMKNVVEQMHEDIISLMDQSLKPC-----VKITP 124
 QY 65 LVNFGNVLOEIFTDEARTGOENNLGEG-KNGVYTCFPRDCLPKGS-----FEELPY 116
 DB 125 ICVTLLN--CSDVNTNTNTSSWENMGGEIKN---CSFNITTSIGKKVRKDYALFNRLDV 178
 QY 117 SP-EIPPRKQYLRSRMPEGTRPEAKEQLFSGGSLVPHLC 157
 DB 179 VPIDNAKNTTSMINCNTSVITQACPKISFEP--IPHYC 217

RESULT 9

Q75939 PRELIMINARY; PRT; 501 AA.
 AC Q75939;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DB (Clone B1BR002W.0102aED) proviral 5' ORF (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brazil;
 RA Ranjbar S., Holmes H.;
 RT "Molecular Characterization of HIV-1 isolate from Brazil."
 DR EMBL; L35493; AAA72447.1; -
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 501
 SQ SEQUENCE 501 AA; 56483 MW; 36291BA1BFED54CB CRC64;

RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L35490; AAA72445.1; -
 DR InterPro: IPR000777; GP120.
 KW Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 501
 SQ SEQUENCE 501 AA; 56498 MW; 218F6822A5AF5B31 CRC64;

Query Match 10.2%; Score 104; DB 15; Length 501;
 Best Local Similarity 24.0%; Pred. No. 0.16; 71; Indels 36; Gaps 9;
 Matches 40; Conservative 25; Mismatches 66; Indels 36; Gaps 9;

QY 7 THLCWPTVPNPAESSIATWGGDDFKDKLNLKES-----DVSNTEDRIILKPCSTPDK 59
 DB 71 THACVPTDPNPGQEVVLENTYENFMNMKNVVEQMHEDIISLMDQSLKPC-----119
 QY 60 LVYDKLVNFGNVLOEIFTDEARTGOENNLGEG-KNGVYTCFPRDCLPKGS-----F 111
 DB 120 VKITPICYTLN--CSDVNTNTNTSSWENMGGEIKN---CSFNITTSIGKKVRKDYALF 173
 QY 112 EELPYSP-EIPPRKQYLRSRMPEGTRPEAKEQLFSGGSLVPHLC 157
 DB 174 NRLDVVPIDNAKNTTSMINCNTSVITQACPKISFEP--IPHYC 217

RESULT 10

Q75937 PRELIMINARY; PRT; 501 AA.
 AC Q75937;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DB (Clone B1BR002W.01012aED) proviral 5' ORF (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Brazil;
 RA Ranjbar S., Holmes H.;
 RT "Molecular Characterization of HIV-1 isolate from Brazil."
 RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L35489; AAA72444.1; -
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 501
 SQ SEQUENCE 501 AA; 56427 MW; B6BEC500741883A5 CRC64;

Query Match 10.1%; Score 103; DB 15; Length 501;
 Best Local Similarity 25.3%; Pred. No. 0.2; 71; Indels 26; Gaps 8;
 Matches 41; Conservative 24; Mismatches 71; Indels 26; Gaps 8;
 QY 7 THLCWPTVPNPAESSI--ATWGGDDFKDKLNLKESDVSNTEDRIILKPCSTPDKLVYDK 64
 DB 71 THACVPTDPNPGQEVVLENTYENFMNMKNVVEQMHEDIISLMDQSLKPC-----VKITP 124
 QY 65 LVNFGNVLOEIFTDEARTGOENNLGEG-KNGVYTCFPRDCLPKGS-----FEELPY 116
 DB 125 ICVTLLN--CSDVNTNTNTSSWENMGGEIKN---CSFNITTSIGKKVRKDYALFNRLDV 178
 QY 117 SP-EIPPRKQYLRSRMPEGTRPEAKEQLFSGGSLVPHLC 157
 DB 179 VPIDNAKNTTSMINCNTSVITQACPKISFEP--IPHYC 217

RESULT 11

Q75942 PRELIMINARY; PRT; 501 AA.
 AC Q75942;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

OX NCB1_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=94CV42-10e;
 RA Gao F., Vidal N., Li Y., Traak S.A., Chen Y., Kostrikis L.G., Ho D.D.,
 RA Kim J., Choe K., Oh M.-D., Salminen M., Robertson D.L., Shaw G.M.,
 RA Hahn B.H., Peeters M.;
 RT "Evidence for two distinct sub-subtypes within the HIV-1 subtype A
 RT radiation";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF286249; AAK82673.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 865 AA; 97687 MW; C32E79B7EA71F3C CRC64;

Query Match 9.8%; Score 99.5; DB 15; Length 865;
 Best Local Similarity 24.1%; Pred. No. 0.89; Mismatches 69; Indels 65; Gaps 10;
 Matches 49; Conservative 20;

QY 7 THLCWPTVPNPASSIAVHGDDEKDLNLES--DQSVNTEEDRIILKPC----- 53
 DB 67 THACVPTDPNPQEIHLNVNTEFNFMNMKNMVEQMHEDIISLMDQSLKPCVKTPLCVTLN 126
 QY 54 -----STPSDKL-----VIDKLVNFGNV-----LOEITDEARTGOEN 87
 DB 127 CSNANVSSTPNDAISTPPGEIKNCSYVVTTERIDKTONVHSLFYRLDVQIDESK--NEN 184
 QY 88 NLGGEKNQY--VVC---PFRDPCPLGKSPFELVPSPEIPRKSQYLRSME----- 134
 DB 185 TSSSSNTMYRLINCNTSTTQACP-KITEPIPIH-YCAPAGFALLKCKDPERNGTGSCK 242
 QY 135 -----GTRPEAKQQLFSG 148
 DB 243 NVSSVQCTHGIGKFPVSTQLLNG 265

RESULT 15
 Q99BY1 PRELIMINARY; PRT; 800 AA.
 ID Q99BY1;
 AC Q99BY1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCB1_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suthent R., Srisurapanon S.;
 RT "Biological and immunological characteristics of HIV-1 subtype E in
 RT cerebrospinal fluid and blood";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF322201; AAK09408.1; -
 DR InterPro; IPR000328; Env_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 FT NON_TER 1
 SQ SEQUENCE 800 AA; 90879 MW; BBBFOC3791E2B38C CRC64;

Query Match 9.7%; Score 99; DB 15; Length 800;
 Best Local Similarity 20.2%; Pred. No. 0.9; Mismatches 77; Indels 88; Gaps 11;
 Matches 50; Conservative 32; Mismatches 77; Indels 88; Gaps 11;
 QY 7 THLCWPTVPNPASSI--ATWHDGDFDKLNLKESDQSVNTEEDRIILKPC--STP----- 56

DB 18 THACVPTDPNPQEIHLNVNTEFNFMNMKNMVEQMHEDIISLMDQSLKPCVKTPLCVTLN 77
 QY 57 -----SKLVYDKL--VNFENVLQEI-----FTD 79
 DB 78 CVDARKNDSNIIKNTDTARIGNIDEVANCSENNTEIIDKQAYALFYRLDIAPIED 137
 QY 80 EARTGOENNLGGEKNQYVTC---PFRDPCPLGKSPFELVPSPEIP----- 121
 DB 138 DHTISKYNSNENYRLINCNSIITQACP-KISFPIPIHYCTPAGYAILKCNDRNG 196
 QY 122 PRKSQYLRS-RMPEGTRPEAKQQLFSGQSLVPHLCEGAPNPYLNKSVTAREFLV-SE 179
 DB 197 DRPCKNVSQCTHGIGKFPVSTQLLNG-----SLAEETIIIRSE 236
 QY 180 KLPERTK 186
 DB 237 MLTNNAK 243

Search completed: August 18, 2003, 13:30:20
 Job time : 70.8907 secs

DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE (Clone B1BR002W.01052AED) proviral 5' ORF (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brazil;
RA Ranjbar S., Holmes H.;
RT "Molecular Characterization of HIV-1 isolate from Brazil."
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: L35491; AAA72446.1;
DR InterPro: IPR007777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 501 501
SQ SEQUENCE 501 AA; 56427 MW; B6BEC500741883A5 CRC64;

Query Match 10.1%; Score 103; DB 15; Length 501;
Best Local Similarity 25.3%; Pred. No. 0.2;
Matches 41; Conservative 24; Mismatches 71; Indels 26; Gaps 8;

QY 7 THLCWPTVNPASSI--ATWHDGDKDKLANKESDVSNTEDRIKPCSTSDKLVYK 64
DB 71 THACVPTDNPQVLENTENFNMMKNVBEQMHEDIISLMDQSLKPC-----VKITP 124
QY 65 LVNFGNVLQELFTDEARTGOENLGE--KNGVYTCPPRPDCLGK-----PEELPV 116
DB 125 ICVTLL--CSDVNTTNTTNSWENMGELK-----CSFNITISIGKVKADVALFPRRLV 178
QY 117 SP-EIPRKSQYLRSMPEGTPEAKEQLLFSQSLVPHLC 157
DB 179 VPIDNAKNTTSYMLINCNTSVITQACPISFEP---IPHYC 217

RESULT 12

Q99BX1 PRELIMINARY; PRT; 791 AA.
AC Q99BX1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Sutent R., Sistruppanon S.;
RT "Biological and immunological characteristics of HIV-1 subtype B in cerebrospinal fluid and blood";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A332211; AAK09418.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 1 1
FT NON_TER 791 791
SQ SEQUENCE 791 AA; 89550 MW; A2C337158E9871FB CRC64;

Query Match 10.1%; Score 102.5; DB 15; Length 791;
Best Local Similarity 21.3%; Pred. No. 0.41;
Matches 51; Conservative 34; Mismatches 73; Indels 81; Gaps 13;

QY 7 THLCWPTVNPASSI--ATWHDGDKDKLANKESDVSNTEDRIKPC--STP----- 56
DB 18 THACVPTDNPQVLENTENFNMMKNVBEQMHEDIISLMDQSLKPCVLTPLCTILN 77
QY 57 -SDKLVIDKLNVN-----FGNVLOEI-----FTDEARTGOEN-----NLGE 92

DB 78 CVDANKLNSINIITDEARIGNISDEVNCSFNITTELDKKQKHALFRLDIKIGND 137
QY 93 KNG-----YVTCP---FRDPCPLGKSPPELVSPPEIPRKSQYLR----- 130
DB 138 NNSREYRLINCNSIITQACP-KISFDPIPH-YCTPAGYAFKCKNDKFKNGTGPCKNVS 195
QY 131 --RMEGTREPAKEQLLFSQSLVPHLCSEGAPNPYLNSTYAREFLV-SEKLPEHTK 186
DB 196 SVQCTHGKIPVYSTQLLLNG-----SLAEELIIRSENLANNAK 234

RESULT 13

Q74304 PRELIMINARY; PRT; 515 AA.
AC Q74304;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE Envelope glycoprotein gp120 (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Ray S.C., Lubaki N.M., Dhruva B.R., Siliciano R.F., Bollinger R.C.;
RT "Strain-specific Cytolytic T Lymphocyte responses directed against
RL Human immunodeficiency virus type 1 env.";
DR Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: L78831; AAB02635.1;
DR InterPro: IPR007777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 515 515
SQ SEQUENCE 515 AA; 57626 MW; 5AF783BA2498A619 CRC64;

Query Match 9.8%; Score 100; DB 15; Length 515;
Best Local Similarity 23.9%; Pred. No. 0.41;
Matches 58; Conservative 23; Mismatches 100; Indels 62; Gaps 9;

QY 7 THLCWPTVNPASSI--ATWHDGDKDKLANKESDVSNTEDRIKPC--STP----- 56
DB 70 THACVPTDNPQVLENTENFNMMKNVBEQMHEDIISLMDQSLKPCVLTPLCTILN 129
QY 57 -SDKLVIDKLNVNFGNVLQELFT-----DEARTGOENLGEKNGVYTC 100
DB 130 CSDYKANDTNTTEIANCSFNITNTIRKQVEYALFYKIDVVPIDGNDSTRYRLSCNTSV 189
QY 101 FRDPCPLGKSPPELVSPPEIPR-----KSQYLRSM-----EGTPEAKEQL 144
DB 190 ITQACP-KVSEPIPIHICAPGAILKCKDKKFKNGTGPCKNVSTVQCTHGIRPVSTOL 248
QY 145 LFSQSLVPHD-----HCEBEGAPNPYLNSTYAREFLVSEKLPETHK 186
DB 249 ILNG-SLAEEVVRSENFNTNNAKTIIVQLNESVAINCIRBNNTKSIHIGRAFYTT 307
QY 187 GEV 189
DB 308 GEV 310

RESULT 14

Q90QW8 PRELIMINARY; PRT; 865 AA.
AC Q90QW8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:12:37 ; Search time 9.12114 Seconds
(without alignments)
417.649 Million cell updates/sec

Title: US-09-892-949-2_COPY_520_543
Perfect score: 109
Sequence: 1 ILITSLIGGGULLILITLTVAYGL 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_19Jun03.*
2: /SIDSL/gcgcdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgcdata/geneseq/geneseq-emb1/AA1981.DAT.*
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20: /SIDSL/gcgcdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgcdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgcdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgcdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	581	ABP54367	Human NR10.6 splic
2	109	100.0	620	ABG05070	Novel human diagn
3	109	100.0	627	ABP54366	Human NR10.5 splic
4	109	100.0	649	ABG05738	Human zcyfor17 pro
5	109	100.0	652	ABBS1242	Human haemopoietin
6	109	100.0	652	AAE24028	Human HPRI variant
7	109	100.0	662	ABBS1244	Human haemopoietin
8	109	100.0	662	AAE24029	Human HPRI variant
9	109	100.0	662	ABG05741	Human zcyfor17 pro

10	109	100.0	681	24	ABP54363
11	109	100.0	732	23	ABG05730
12	109	100.0	745	23	AAE24024
13	109	100.0	764	24	ABP54366
14	109	100.0	764	24	ABP54365
15	83	76.1	662	23	ABG05742
16	83	76.1	716	24	ABP54370
17	83	76.1	716	24	ABP54371
18	82	75.2	726	23	AAE24037
19	52	47.7	795	22	ABG62996
20	51	46.8	302	23	ABJ03986
21	51	46.8	318	22	AAU24652
22	51	46.8	318	22	AAU24652
23	51	46.8	318	23	ABP95651
24	51	46.8	318	23	ABJ04725
25	51	46.8	318	23	AAU95704
26	51	46.8	318	23	AAU85272
27	51	46.8	318	24	ABR01682
28	51	46.8	318	24	ABU11168
29	50	45.9	314	23	AAE25071
30	50	45.9	325	23	ABP51564
31	49.5	45.4	363	22	AAU91861
32	49	45.0	25	18	AAW34001
33	49	45.0	92	20	AAW97363
34	49	45.0	116	21	AAU01911
35	49	45.0	270	23	ABP95678
36	49	45.0	313	22	AAU71830
37	49	45.0	324	23	AAU48227
38	49	45.0	337	15	AAK53753
39	49	45.0	337	19	AAW48734
40	49	45.0	337	21	AAW21698
41	49	45.0	337	23	AAU91240
42	49	45.0	352	13	AAU27792
43	49	45.0	352	16	AAK68812
44	49	45.0	352	16	AAK80757
45	49	45.0	352	20	AAU39993

ALIGNMENTS

RESULT 1
ABP54367
ID ABP54367 standard; Protein; 581 AA.
AC ABP54367;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.6 splicing variant protein SEQ ID NO:10.
XX
KW NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation.
XX
OS Homo sapiens.
XX
EN WO200277230-A1.
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-UP02769.
XX
PR 26-MAR-2001; 2001JP-0087298.
XX
(CHUS) CHUGAI SEIYAKU KK.
XX
PA Maeda M, Yaguchi N, Hasegawa M;
PI WPI, 2003-018925/01.
XX
DR N-PSDB; ABG83367.
XX
PT NR10 splicing variants of haematopoietin receptor proteins and encoded

PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -
PS Claim 1; Fig 13-15; 250pp; Japanese.
XX
CC The present invention describes hematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC hematopoietic factors, and developing remedies for immunological and
CC hematopoietic diseases. The haematopoietin receptor genes participate
CC in vivo immunomodulation and hematopoietic cell regulation, and in
CC the search for hematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.6
CC protein from the present invention.
XX
SQ Sequence 581 AA;
Query Match 100.0%; Score 109; DB 24; Length 581;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILITSLIGGGLLILITLVAYGL 24
Db 552 IILITSLIGGGLLILITLVAYGL 575
RESULT 2
ABG05070
ID ABG05070 standard; Protein; 620 AA.
XX
AC ABG05070;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #5061.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS69257.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 35429; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polynucleotide chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 620 AA;
Query Match 100.0%; Score 109; DB 22; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IILITSLIGGGLLILITLVAYGL 24
Db 408 IILITSLIGGGLLILITLVAYGL 431
RESULT 3
ABP54366
ID ABP54366 standard; Protein; 627 AA.
XX
AC ABP54366;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human NR10.5 splicing variant protein SEQ ID NO:8.
XX
KW NR10; splicing variant; haematopoietin receptor; immunomodulator;
KW haemostatic; hematopoietic factor; immunological disease;
KW hematopoietic disease; hematopoietic cell regulation.
XX
OS Homo sapiens.
XX
PN WO200277230-A1.
XX
PD 03-OCT-2002.
XX
PF 22-MAR-2002; 2002WO-JP02769.
XX
PR 26-MAR-2001; 2001JP-0087298.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Maeda M, Yaguchi N, Hasegawa M;
XX
DR WPI; 2003-018925/01.
DR N-PSDB; ABG83366.
XX
PT NR10 splicing variants of haematopoietin receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -
XX
PS Claim 1; Fig 10-12; 250pp; Japanese.
XX
CC The present invention describes hematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC hematopoietic factors, and developing remedies for immunological and
CC hematopoietic diseases. The haematopoietin receptor genes participate
CC in vivo immunomodulation and hematopoietic cell regulation, and in
CC the search for hematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.5
CC protein from the present invention.
XX
SQ Sequence 627 AA;

Query Match 100.0%; Score 109; DB 24; Length 627;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILITSLIGGGILLITLVAYGL 24
 Db 552 ILITSLIGGGILLITLVAYGL 575

RESULT 4
 ABB05738
 ID ABB05738 standard; Protein; 649 AA.

AC ABB05738;
 DT 01-MAY-2002 (first entry)

DE Human zcytor17 protein sequence SEQ ID NO:46.

XX Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 XX antiinflammatory; antiviral; antirheumatic; antiallergic; cytoskeletal;
 XX muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 XX infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 XX autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 XX inflammatory disease; pancreatitis; inflammatory bowel disease.

OS Homo sapiens.

PN WO200200721-A2.

PD 03-JAN-2002.

PF 26-JUN-2001; 2001WO-US20484.

PR 26-JUN-2000; 2000US-214282P.

PR 29-JUN-2000; 2000US-214955P.

PR 08-FEB-2001; 2001US-267963P.

PA (ZYMO) ZYMOGENETICS INC.

PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;

PI Maurer MF;

DR N-PSDB; ABA93803.

PT Isolated polynucleotide encoding a cytokine receptor zcytor17 which is

PT useful for treating and diagnosing lymphoid, immune, inflammatory,

PT splenic, blood or bone disorders -

PS Claim 18; Page 195-197; 235pp; English.

XX The present invention describes a cytokine receptor designated zcytor17.
 CC Zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 CC antirheumatic, antiallergic and muscular activities. The zcytor17
 CC proteins are useful for treating and diagnosing lymphoid, immune,
 CC inflammatory, splenic, blood or bone disorders. Agonists or
 CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
 CC immunity and for stimulating lymphocyte proliferation, such as in the
 CC treatment of infections involving immunosuppression, including certain
 CC viral infections. They are also useful for inducing cytotoxicity and
 CC for treating leukopenias. Antagonists of zcytor17 polypeptides are useful
 CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention.

SO Sequence 649 AA;

Query Match 100.0%; Score 109; DB 23; Length 649;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILITSLIGGGILLITLVAYGL 24
 Db 520 ILITSLIGGGILLITLVAYGL 543

RESULT 5
 AAB51242
 ID AAB51242 standard; Protein; 652 AA.

AC AAB51242;

DT 26-MAR-2001 (first entry)

DE Human haemopoietin receptor protein NR10.1 SEQ ID NO:2.

XX Human; haemopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
 XX immunoregulation; haematopoietic cell regulation; transmembrane;
 XX immune disorder; haematopoietic disorder; autoimmune disease; allergy;
 XX metal allergy; pollen allergy.

OS Homo sapiens.

PN WO200075314-A1.

PD 14-DEC-2000.

PF 01-JUN-2000; 2000WO-JP03556.

PR 02-JUN-1999; 99JP-0155797.

PR 30-JUL-1999; 99JP-0217797.

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

PI Maeda M, Yaguchi N;

PI WPI; 2001-061720/07.

DR N-PSDB; AAC92337.

PT Hematopoietin receptor protein NR10 for screening potential ligands for

PT treatment of immune and hematopoietic disorders such as autoimmune

PT diseases and allergies -

PS Claim 1; Fig 3-5; 127pp; Japanese.

XX The present sequence represents a human haemopoietin receptor protein
 CC (NR10), specifically designated NR10.1. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haemopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell
 CC regulation in vivo, and is useful in searching for haematopoietic
 CC factors capable of binding to the receptor. NR10 can be used for the
 CC identification of substances for the treatment and prevention of immune
 CC and haematopoietic disorders including autoimmune diseases and allergies
 CC such as metal and pollen allergy.

SO Sequence 652 AA;

Query Match 100.0%; Score 109; DB 22; Length 652;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ILITSLIGGGILLITLVAYGL 24
 Db 533 ILITSLIGGGILLITLVAYGL 556

RESULT 6
 AAE24028
 ID AAE24028 standard; Protein; 652 AA.

AC AAE24028;

DT 23-SEP-2002 (first entry)
 XX
 DE Human HPRI variant protein #2.
 XX
 KW Human; haematopoietin receptor; receptor; HPRI; HPR2; cell proliferation;
 KW pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
 KW neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
 KW cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 KW ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 KW osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;
 KW anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 KW demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 KW vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 KW stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 KW ischaemic disease; variant.
 XX
 OS Homo sapiens.
 XX
 PN WO200229060-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31634.
 XX
 PR 06-OCT-2000; 2000US-238706P.
 XX
 PR 13-OCT-2000; 2000US-240476P.
 XX
 PR 20-FEB-2001; 2001US-270282P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
 XX
 PI WPI; 2002-330172/36.
 XX
 PT Human and murine haematopoietin receptor polypeptides HPRI and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 PT hormone related conditions -
 XX
 PS Disclosure; Page 110-112; 136pp; English.
 XX
 CC The present invention relates to human and murine haematopoietin receptor
 CC polypeptides HPRI and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukaemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various haematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCC and NSCC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC squamous cell carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polynuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC myasthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischaemic diseases. HPRI and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence
 CC is human HPRI variant protein.

SQ Sequence 652 AA;
 Query Match 100.0%; Score 109; DB 23; Length 652;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILITSLIGGGLIIITLVAYGL 24
 |||||
 DB 533 ILITSLIGGGLIIITLVAYGL 556
 |||||
 RESULT 7
 AAB51244
 ID AAB51244 standard; Protein; 662 AA.
 XX
 AC AAB51244;
 XX
 DT 26-MAR-2001 (first entry)
 XX
 DE Human haematopoietin receptor protein NR10.3 SEQ ID NO:17.
 XX
 KW Human; haematopoietin receptor; NR10.1; NR10.2; NR10.3; NR10;
 KW immunoregulation; haematopoietic cell regulation; transmembrane;
 KW immune disorder; haematopoietic disorder; autoimmune disease; allergy;
 KW metal allergy; pollen allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200075314-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-JP03556.
 XX
 PR 02-JUN-1999; 99JP-0155797.
 XX
 PR 30-JUL-1999; 99JP-0217797.
 XX
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 XX
 PI Maeda M, Yaguchi N;
 XX
 DR WPI; 2001-061720/07.
 XX
 DR N-PSDB; AAC92350.
 XX
 PT Haematopoietin receptor protein NR10 for screening potential ligands for
 PT treatment of immune and hematopoietic disorders such as autoimmune
 PT diseases and allergies -
 XX
 PS Claim 1; Fig 13-14; 127pp; Japanese.
 XX
 CC The present sequence represents a human haematopoietin receptor protein
 CC (NR10), specifically designated NR10.3. NR10 occurs as a transmembrane
 CC protein and a soluble protein. NR10 is a haematopoietin receptor molecule
 CC which participates in immunoregulation and haematopoietic cell
 CC regulation in vivo, and is useful in searching for haematopoietic
 CC factors capable of binding to the receptor. NR10 can be used for the
 CC identification of substances for the treatment and prevention of immune
 CC and haematopoietic disorders including autoimmune diseases and allergies
 CC such as metal and pollen allergy.
 XX
 SQ Sequence 662 AA;
 Query Match 100.0%; Score 109; DB 22; Length 662;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ILITSLIGGGLIIITLVAYGL 24
 |||||
 DB 533 ILITSLIGGGLIIITLVAYGL 556
 |||||
 RESULT 8
 AAB24029

AAE24029 standard; Protein; 662 AA.
 AAE24029;
 23-SEP-2002 (first entry)
 Human HPR1 variant protein #3.
 Human; haematopoietin receptor; HPR1; HPR2; cell proliferation;
 pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
 neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
 cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 osteoclast disorder; periodontitis; acute polymyopathy; Bell's palsy;
 anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease;
 demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 ischaemic disease; variant.
 Homo sapiens.
 MO200229060-A2.
 11-APR-2002.
 05-OCT-2001; 2001WO-US31634.
 06-OCT-2000; 2000US-238706P.
 13-OCT-2000; 2000US-240476P.
 20-FEB-2001; 2001US-270282P.
 (IMMW) IMMUNEX CORP.
 Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR;
 WPI; 2002-330172/36.
 Human and murine hematopoietin receptor polypeptides HPR1 and HPR2,
 useful for treating cell proliferation, metabolic, and reproductive
 hormone related conditions -
 Disclosure; Page 112-115; 136pp; English.
 The present invention relates to human and murine hematopoietin receptor
 polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 treating cell proliferation conditions e.g., pancytopenia, leukopenia,
 anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 resulting from a lack of bone-forming cells. They are also useful for
 treating cell proliferation conditions such as leukaemia and tumour
 metastasis, osteoporosis resulting from an excess of bone-resorbing
 cells. HPR sequences are also useful for treating medical conditions and
 diseases such as cell proliferation, metabolic and reproductive hormone
 related conditions. They are useful for treating various haematologic and
 oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
 cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
 of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 dysplastic syndromes (including refractory anaemia, refractory anaemia
 with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 myeloid metaplasia, osteoclast disorders that lead to bone loss such
 as osteoporosis including post-menopausal osteoporosis, periodontitis
 resulting in tooth loosening or loss, prosthesis loosening after joint
 replacement, neurodegenerative conditions (e.g., acute polymyopathy,
 Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 dementia including Creutzfeld-Jacob disease, demyelinating neuropathy,
 Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 myasthenia gravis, chronic neuronal degeneration, stroke including
 cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful

for treating various other disorders such as osteoporosis, obesity,
 deficient mammary development and infertility. The present sequence
 is human HPR1 variant protein.
 SEQ Sequence 662 AA;
 Query Match 100.0%; Score 109; DB 23; Length 662;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 ILLITSLGGGILLITITVAYGL 24
 533 ILLITSLGGGILLITITVAYGL 556
 RESULT 9
 ABB05741 standard; Protein; 662 AA.
 ABB05741;
 01-MAY-2002 (first entry)
 Human zcytor17 protein sequence SEQ ID NO:54.
 zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
 antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
 muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
 infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
 autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 inflammatory disease; pancreatitis; inflammatory bowel disease.
 Homo sapiens.
 WO200200721-A2.
 03-JAN-2002.
 26-JUN-2001; 2001WO-US20484.
 26-JUN-2000; 2000US-214282P.
 29-JUN-2000; 2000US-214955P.
 08-FEB-2001; 2001US-267963P.
 (Zymo) ZYMOGENETICS INC.
 Sprecher CA, Preenell SR, Gao Z, Whitmore TE, Kuiper JL;
 Maurer MF;
 WPI; 2002-090519/12.
 N-PSDB; ABA93808.
 Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
 useful for treating and diagnosing lymphoid, immune, inflammatory,
 splenic, blood or bone disorders -
 Example 1; Page 204-206; 235pp; English.
 The present invention describes a cytokine receptor designated zcytor17.
 zcytor17 has immunomodulatory, antiinflammatory, antiviral, cytostatic,
 antirheumatic, antiarthritic and muscular activities. The zcytor17
 proteins are useful for treating and diagnosing lymphoid, immune,
 inflammatory, splenic, blood or bone disorders. Agonists or
 anti-zcytor17 antibodies are useful in stimulating cell-mediated
 immunity and for stimulating lymphocyte proliferation, such as in the
 treatment of infections involving immunosuppression, including certain
 viral infections. They are also useful for inducing cytotoxicity and
 for treating leukopneias. Antagonist of zcytor17 polypeptides are useful
 for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 pancreatitis, and inflammatory bowel disease. zcytor17 was mapped to
 chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 ABA93843 and ABB05730 to ABB05745 represent sequences used in the

CC exemplification of the present invention.
XX
SQ Sequence 662 AA;

Query Match 100.0%; Score 109; DB 23; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITVAAYGL 24
DB 533 IILITSLIGGGLIILITVAAYGL 556

RESULT 10
ABP54363
ID ABP54363 standard; Protein; 661 AA.

AC ABP54363;

DT 20-JAN-2003 (first entry)

XX Human NR10.3 splicing variant protein SEQ ID NO:2.

XX NR10; splicing variant; haematopoietic receptor; immunomodulator;
KW haemostatic; haematopoietic factor; immunological disease;
KW haematopoietic disease; haematopoietic cell regulation.

XX Homo sapiens.

XX WO200277230-A1.

XX 03-OCT-2002.

XX 22-MAR-2002; 2002WO-JP02769.

XX 26-MAR-2001; 2001JP-0087298.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Maeda M, Yaguchi N, Hasegawa M;

XX WPI; 2003-018925/01.

XX N-PSDB; ABQ83363.

XX NR10 splicing variants of hematopoietic receptor proteins and encoded
PT genes, applicable in searching hematopoietic factors and developing
PT remedies for immunological and hematopoietic diseases -

XX Example 2; Fig 3; 250pp; Japanese.

XX The present invention describes haematopoietic receptor NR10 splicing
CC variants (I). (I) have immunomodulator and haemostatic activities. The
CC proteins and encoded genes are applicable in searching for novel
CC haematopoietic factors, and developing remedies for immunological and
CC haematopoietic diseases. The haematopoietic receptor genes participate
CC in *in vivo* immunomodulation and haematopoietic cell regulation, and in
CC the search for haematopoietic factors capable of functionally binding
CC to the receptors. The present sequence represents the human NR10.3
CC protein from the present invention.

XX Sequence 681 AA;

Query Match 100.0%; Score 109; DB 24; Length 681;

Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITVAAYGL 24
DB 552 IILITSLIGGGLIILITVAAYGL 575

RESULT 11

ABP05730

ID ABB05730 standard; Protein; 732 AA.

XX ABB05730;

XX 01-MAY-2002 (first entry)

XX Human zcytor17 protein sequence SEQ ID NO:2.

XX Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antinflammatory; antiviral; antineutrophic; antirheumatic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease.

XX Homo sapiens.

XX WO200200721-A2.

XX 03-JAN-2002.

XX 26-JUN-2001; 2001WO-US20484.

XX 26-JUN-2000; 2000US-214282P.

XX 29-JUN-2000; 2000US-214955P.

XX 08-FEB-2001; 2001US-267963P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Pressnell SR, Gao Z, Whitmore TE, Kuljper JL;

XX Maurer ME;

XX WPI; 2002-090519/12.

XX N-PSDB; ABA93767.

XX Claim 18; Page 166-168; 235pp; English.

XX The present invention describes a cytokine receptor designated zcytor17.
CC zcytor17 has immunomodulatory, antinflammatory, antiviral, cytostatic,
CC antirheumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or
CC anti-zcytor17 antibodies are useful in stimulating cell-mediated
CC immunity and for stimulating lymphocyte proliferation, such as in the
CC treatment of infections involving immunosuppression, including certain
CC viral infections. They are also useful for inducing cytotoxicity and
CC for treating leukopenias. Antagonists of zcytor17 polypeptides are useful
CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
CC exemplification of the present invention.

XX Sequence 732 AA;

Query Match 100.0%; Score 109; DB 23; Length 732;

Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITVAAYGL 24
DB 520 IILITSLIGGGLIILITVAAYGL 543

RESULT 12

AAE24024
ID AAE24024 standard; Protein; 745 AA.

XX

AAE24024;
 23-SEP-2002 (first entry)
 Human haematopoietin receptor 1 (HPR1) protein.
 Human; haematopoietin receptor; HPR1; HPR2; cell proliferation;
 pancytopenia; leucopenia; anaemia; thrombocytopenia; osteoporosis;
 neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
 cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
 ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
 osteoclast disorder; periodontitis; acute polynuropathy; Bell's palsy;
 anorexia nervosa; chronic fatigue syndrome; Creutzfeldt-Jacob disease;
 demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
 vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
 stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
 ischemic disease.
 Homo sapiens.
 Location/Qualifiers
 20..32
 /label= Signal_peptide
 33..745
 /note= "Human mature HPR1 protein"
 33..241
 /note= "Cytokine receptor domain"
 83
 /note= "This residue changes to Ala during
 allelic variation"
 135..138
 /note= "Proline-rich linker"
 139..241
 /note= "C-terminal cytokine receptor subdomain"
 168
 /note= "This residue changes to Asn during
 allelic variation"
 187
 /note= "This residue changes to Thr during
 allelic variation"
 224..228
 /note= "MSXMS motif"
 242..515
 /note= "Fibronectin repeat"
 361
 /note= "This residue changes to Pro during
 allelic variation"
 362
 /note= "This residue changes to Gly during
 allelic variation"
 510
 /note= "This residue changes to Asn during
 allelic variation"
 517
 /note= "Encoded by GAC; This residue changes to
 Asp during allelic variation"
 526..556
 /note= "Extended transmembrane domain"
 533..552
 /note= "Core transmembrane domain"
 553..745
 /note= "Cytoplasmic domain"
 563..573
 /note= "Box1 conserved motif"
 588..592
 /note= "Repeat peptide"
 597..601
 /note= "Repeat peptide"
 603..607
 /note= "Repeat peptide"
 614..618
 /note= "Repeat peptide"
 619..623

FT Domain /note= "Repeat peptide"
 631..641
 /note= "Box2 conserved motif"
 FT Region 635..639
 /note= "Repeat peptide"
 FT Misc-difference 679
 /note= "This residue changes to Gly during
 allelic variation"
 PN MO200229060-A2.
 PD 11-APR-2002.
 PP 05-OCT-2001; 2001WO-US31634.
 PR 06-OCT-2000; 2000US-238706P.
 PR 13-OCT-2000; 2000US-240476P.
 PR 20-FEB-2001; 2001US-270282P.
 XX (IMMW) IMMUNEX CORP.
 PA Cosman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR.
 PI WPI; 2002-330172/36.
 DR N-PSDB; AAD38772.
 XX Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,
 PT useful for treating cell proliferation, metabolic, and reproductive
 XX hormone related conditions -
 XX Claim 1; Page 84-87; 136pp; English.
 XX The present invention relates to human and murine haematopoietin receptor
 CC polypeptides HPR1 and HPR2. Sequences of the invention are useful for
 CC treating cell proliferation conditions e.g., pancytopenia, leucopenia,
 CC anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
 CC resulting from a lack of bone-forming cells. They are also useful for
 CC treating cell proliferation conditions such as leukaemia and tumour
 CC metastasis, osteoporosis resulting from an excess of bone-resorbing
 CC cells. HPR sequences are also useful for treating medical conditions and
 CC diseases such as cell proliferation, metabolic and reproductive hormone
 CC related conditions. They are useful for treating various haematologic and
 CC oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
 CC carcinoma, myelogenous leukaemia, colon, stomach, prostate, renal cell,
 CC cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
 CC cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
 CC sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
 CC squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
 CC of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
 CC dysplastic syndromes (including refractory anaemia, refractory anaemia
 CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
 CC penic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
 CC myeloid metaplasia, osteoclast disorders that lead to bone loss such
 CC as osteoporosis including post-menopausal osteoporosis, periodontitis
 CC resulting in tooth loosening or loss, prosthesis loosening after joint
 CC replacement, neurodegenerative conditions (e.g., acute polynuropathy,
 CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
 CC dementia including Creutzfeldt-Jacob disease, demyelinating neuropathy,
 CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
 CC myasthenia gravis, chronic neuronal degeneration, stroke including
 CC cerebral ischemic diseases. HPR1 and HPR2 polypeptides are also useful
 CC for treating various other disorders such as osteoporosis, obesity,
 CC deficient mammary development and infertility. The present sequence
 CC is human HPR1 protein.
 XX
 SQ Sequence 745 AA;

Query Match 100.0%; Score 109; DB 23; Length 745;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 IILITSLIGGLIIIIITVAYGL 24
 |||

```

DB      533 ILITSLIGGGLIILITLVAVGL 556

RESULT 13
ABP54364
ID      ABP54364 standard; Protein; 764 AA.
XX
XX      ABP54364;
AC
DT      20-JAN-2003 (first entry)
XX
XX      Human NR10.4 splicing variant protein SEQ ID NO:4.
DE
XX
XX      NR10, splicing variant; haematopoietin receptor; immunomodulator;
KW      haemostatic; haematopoietic factor; immunological disease;
XX      haematopoietic disease; haematopoietic cell regulation.
OS      Homo sapiens.
XX
XX      WO200277230-A1.
PN
XX
XX      03-OCT-2002.
PD
XX
XX      22-MAR-2002; 2002WO-JP02769.
PF
XX
XX      26-MAR-2001; 2001JP-0087298.
PR
XX
XX      (CHUS ) CHUGAI SEIYAKU KK.
PA
XX
XX      Maeda M, Yaguchi N, Hasegawa M;
PI
XX      WPI, 2003-018925/01.
XX      N-PSDB; ABQ83364.
DR
XX
XX      NR10, splicing variants of hematopoietin receptor proteins and encoded
PT      genes, applicable in searching hematopoietic factors and developing
PT      remedies for immunological and hematopoietic diseases
PT
XX
XX      Claim 1; Fig 6; 250pp; Japanese.
XX
XX      The present invention describes haematopoietic receptor NR10 splicing
XX      variants (I). (I) have immunomodulator and haemostatic activities. The
XX      proteins and encoded genes are applicable in searching for novel
XX      haematopoietic factors, and developing remedies for immunological and
XX      haematopoietic diseases. The haematopoietin receptor genes participate
XX      in vivo immunomodulation and haematopoietic cell regulation, and in
XX      the search for haematopoietic factors capable of functionally binding
XX      to the receptors. The present sequence represents the human NR10.4
XX      protein from the present invention.
XX
XX      Sequence      764 AA;
SQ

Query Match      100.0%; Score 109; DB 24; Length 764;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches      24; Conservative      0; Mismatches      0; Indels      0; Gaps      0

QY      1 ILITSLIGGGLIILITLVAVGL 24
      |||||
DB      552 ILITSLIGGGLIILITLVAVGL 575

RESULT 14
ABP54365
ID      ABP54365 standard; Protein; 764 AA.
XX
XX      ABP54365;
AC
XX      20-JAN-2003 (first entry)
DT
XX
XX      Human NR10.4 splicing variant protein SEQ ID NO:6.
DE
XX
XX      NR10, splicing variant; haematopoietin receptor; immunomodulator;
KW      haemostatic; haematopoietic factor; immunological disease;
XX      haematopoietic factor; immunological disease;
XX

```

XX	haematopoietic disease; haematopoietic cell regulation.
XX	
OS	Homo sapiens.
XX	
FN	WO200277230-A1.
XX	
PD	03-OCT-2002.
XX	
FE	22-MAR-2002; 2002WO-JF02769.
XX	
PR	26-MAR-2001; 2001JP-0087298.
XX	
PA	(CHUS) CHUGAI SEIYAKU KK.
XX	
FI	Maeda M, Yaguchi N, Hasegawa M;
DR	WPI; 2003-018925/01.
XX	
DR	N-PSDB; ABQ83365.
XX	
PT	NR10 splicing variants of hematopoietin receptor proteins and encoded
PT	genes, applicable in searching hematopoietic factors and developing
PT	remedies for immunological and hematopoietic diseases
XX	
PS	Claim 1; Fig 7-9; 250pp; Japanese.
XX	
CC	The present invention describes haematopoietic receptor NR10 splicing
CC	variants (1). (1) have immunomodulator and haemostatic activities. The
CC	proteins and encoded genes are applicable in searching for novel
CC	haematopoietic factors, and developing remedies for immunological and
CC	haematopoietic diseases. The haematopoietin receptor genes participate
CC	in in vivo immunomodulation and haematopoietic cell regulation, and in
CC	the search for haematopoietic factors capable of functionally binding
CC	to the receptors. The present sequence represents the human NR10.4
CC	protein from the present invention.
XX	
SQ	Sequence 764 AA;
	Query Match 100.0%; Score 109; DB 24; Length 764;
	Best Local Similarity 100.0%; Pred. No. 1.5e-07;
	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ILLTSLIGGSLILITLVAYGL 24
DB	552 ILLTSLIGGSLILITLVAYGL 575
	RESULT 15
	ABB05742
ID	ABB05742 standard; Protein; 662 AA.
XX	
AC	ABB05742;
XX	
DT	01-MAY-2002 (first entry)
XX	
MO	Mouse zcytor17 protein SEQ ID NO:57.
XX	
XX	Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW	antiinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW	muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW	infection; immunosuppression; cytotoxicity; leukaemia; Crohn's disease;
KW	autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
XX	inflammatory disease; pancreatitis; inflammatory bowel disease.
XX	
OS	Mus musculus.
XX	
PN	WO200200721-A2.
XX	
PD	03-JAN-2002.
XX	
PF	26-JUN-2001; 2001WO-US20484.
XX	
PR	26-JUN-2000; 2000US-214282P.
PR	29-JUN-2000; 2000US-214955P.
XX	

PR 08-FEB-2001; 2001US-267963P.

XX
PA (ZYMO) ZYMOGENETICS INC.
ur

PI Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL,
PI Maurer MF;
...

Maurer MF;

DR WPI; 2002-090519/12.

DR N-PSDB; ABA93810.

PT	Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT	useful for treating and diagnosing lymphoid, immune, inflammatory,
PT	splenic, blood or bone disorders -

splenic, blood or bone disorders -

PS Example 21; Page 212-213; 235pp; English.

XX

CC The present invention describes a cytokine receptor designated zcytor17
CC ZouYor17 has immunomodulatory activity and is a member of the

antirheumatic, antiarthritic and muscular activities. The zcytor17 zcytor17 has immunomodulatory, antitumoral, antilethal, cytostatic,

CC proteins are useful for treating and diagnosing lymphoid, immune,

CC inflammatory, splenic, blood or bone disorders. Agonists or

CC anti-zytor17 antibodies are useful in stimulating cell-mediated

immunity and for stimulating lymphocyte proliferation, such as in the treatment of infectious and immunosuppressive diseases, including certain

CC viral infections. They are also useful for inducing cytotoxicity and CC treatment of infections involving immunosuppression, including certain

CC for treating leukopenias. Antagonist of zcytor17 polypeptides are useful

CC for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple

CC scleriosis), inflammatory diseases (e.g. Crohn's disease), cancer,

pancreatitis, and inflammatory bowel disease. Zcytor1 was mapped to chromosome 5 specifically to the 5c11 chromosomal region AB93767 to

CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the

cc exemplification of the present invention.

3333

SD Sequence 662 AA;

Sequence 662 AA;

Query Match	Score	DB	Length
76.1%	83	23	662

Matches 16: Conservative 5: Mismatches 3
Best Local Similarity 66.7%; Pred. NO. 0.00085;

מס' תיק	שם	מס' תיק	שם
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102	דניאל	103	דניאל
104	דניאל	105	דניאל
106	דניאל	107	דניאל
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152	דניאל	153	דניאל
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188	דניאל	189	דניאל
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194	דניאל	195	דניאל
196	דניאל	197	דניאל
198	דניאל	199	דניאל
200	דניאל	201	דניאל

QY 1 ILLITSLIGGLILITVAYGL 24

[illegible]

Search completed: August 18, 2003, 13:27:02
Job time : 10.1211 secs

Job time : 10.1211 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:24:23 ; Search time 2.96437 Seconds
(without alignments)
342.555 Million cell updates/sec

Title: US-09-892-949-2_COPY_520_543

Perfect score: 109
Sequence: 1 ILLITSLGGGLLIILLTVAYGL 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	45.0	337	1	US-08-153-848-46 Sequence 46, Appl
2	49	45.0	337	3	US-09-299-843A-46 Sequence 46, Appl
3	49	45.0	337	4	US-09-088-337B-46 Sequence 46, Appl
4	49	45.0	337	5	PCT-US93-11153-46 Sequence 46, Appl
5	49	45.0	352	1	US-08-202-056-3 Sequence 3, Appl
6	49	45.0	352	1	US-08-076-093A-4 Sequence 4, Appl
7	49	45.0	352	1	US-08-701-265-4 Sequence 4, Appl
8	49	45.0	352	2	US-08-284-586-4 Sequence 4, Appl
9	49	45.0	352	2	US-08-805-478-4 Sequence 4, Appl
10	49	45.0	352	2	US-08-802-627A-4 Sequence 4, Appl
11	49	45.0	352	2	US-08-801-238-4 Sequence 4, Appl
12	49	45.0	352	2	US-08-801-228-4 Sequence 4, Appl
13	49	45.0	352	3	US-09-104-296-4 Sequence 4, Appl
14	49	45.0	352	4	US-09-517-605-4 Sequence 4, Appl
15	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
16	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
17	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
18	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
19	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
20	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
21	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
22	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
23	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
24	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
25	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
26	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl
27	49	45.0	352	4	US-08-118-270-346 Sequence 4, Appl

28	47	43.1	459	1	US-08-413-118-12 Sequence 12, Appl
29	47	43.1	459	1	US-08-413-118-14 Sequence 14, Appl
30	47	43.1	459	3	US-08-473-446-12 Sequence 12, Appl
31	47	43.1	459	3	US-08-473-446-14 Sequence 14, Appl
32	47	43.1	459	3	US-09-213-053-6 Sequence 2, Appl
33	47	43.1	1394	3	US-09-213-053-2 Sequence 2, Appl
34	46	42.2	92	1	US-08-118-270-341 Sequence 341, App
35	46	42.2	92	5	PCT-US93-08528-341 Sequence 26228, A
36	45	41.3	258	4	US-09-252-991A-26228 Sequence 27195, A
37	45	41.3	296	4	US-09-172-353-2 Sequence 2, Appl
38	45	41.3	370	3	US-09-172-353-3 Sequence 3, Appl
39	45	41.3	370	3	US-09-172-353-7 Sequence 7, Appl
40	45	41.3	370	3	US-08-776-971-140 Sequence 140, App
41	45	41.3	370	3	US-09-799-955-2 Sequence 2, Appl
42	45	41.3	370	4	US-09-799-955-3 Sequence 7, Appl
43	45	41.3	370	4	US-09-799-955-7 Sequence 6288, Ap
44	45	41.3	370	4	US-09-328-352-6288
45	44	40.4	141	4	US-09-328-352-6288

ALIGNMENTS

RESULT 1
US-08-153-848-46
Sequence 46, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwaikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153, 848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-46
Query Match 45.0%; Score 49; DB 1; Length 337;
Best Local Similarity 47.1%; Pred. No. 24;
Matches 8; Conservative 6; Mismatches 0; Gaps 0;

Qy 1 IILITSLIGGGLILIT 17
| : : : : :
Db 32 IIFLTGIVNGVLIVM 48

RESULT 2

US-09-299-843A-46
; Sequence 46, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schwellkart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: J111 E. Un1
; REGISTRATION NUMBER: 43,213
; REFERENCE/DOCKET NUMBER: 27866/32059B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-299-843A-46

Query Match 45.0%; Score 49; DB 3; Length 337;
Best Local Similarity 47.1%; Pred. No. 24;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILIT 17
| : : : : :
Db 32 IIFLTGIVNGVLIVM 48

RESULT 3

US-09-088-337B-46
; Sequence 46, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.

Schwellkart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-088-337B-46

Query Match 45.0%; Score 49; DB 4; Length 337;
Best Local Similarity 47.1%; Pred. No. 24;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILIT 17
| : : : : :
Db 32 IIFLTGIVNGVLIVM 48

RESULT 4

PCT-US93-11153-46
; Sequence 46, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schwellkart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-46

Query Match 45.0%; Score 49; DB 5; Length 337;
Best Local Similarity 47.1%; Pred. No. 24;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILII 17
Db 32 IIFLTGIVNGVLIVM 48

RESULT 5
US-08-202-056-3
Sequence 3, Application US/08202056
Patent No. 5440021
GENERAL INFORMATION:
APPLICANT: Chuntharapal, Anan
APPLICANT: Hebert, Caroline
APPLICANT: Kim, Kyung Jin
APPLICANT: Lee, James
TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,056
FILING DATE: 25-FEB-1994
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids

TYPE: amino acid
TOPOLOGY: linear
US-08-202-056-3

Query Match 45.0%; Score 49; DB 1; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILII 17
Db 47 IIFLTGIVNGVLIVM 63

RESULT 6
US-08-076-093A-4
Sequence 4, Application US/08076093A
Patent No. 5543503
GENERAL INFORMATION:

APPLICANT: Chuntharapal, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PFAA Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-076-093A-4

Query Match 45.0%; Score 49; DB 1; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IILITSLIGGGLILII 17
Db 47 IIFLTGIVNGVLIVM 63

RESULT 7
US-08-701-265-4
Sequence 4, Application US/08701265

Patent No. 5776457
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/701,265
FILING DATE: 22-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-701-265-4
Query Match 45.0%; Score 49; DB 1; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 IILITSLIGGLILILI 17
DB 47 IIFLTIGVNGVILVIM 63
RESULT 8
US-08-284-586-4
Sequence 4, Application US/08284586
Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-284-586-4
Query Match 45.0%; Score 49; DB 2; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 IILITSLIGGLILILI 17
DB 47 IIFLTIGVNGVILVIM 63
RESULT 9
US-08-805-478-4
Sequence 4, Application US/08805478
Patent No. 5874543
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,478
FILING DATE: 25-Feb-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-AUG-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076093
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P0706P2P1C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-805-478-4

Query Match 45.0%; Score 49; DB 2; Length 352;
 Best Local Similarity 47.1%; Pred. No. 25;
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17
 DB 47 IIFLTGIVNGLVILWM 63

RESULT 10
 US-08-802-627A-4
 Sequence 4, Application US/08802627A
 Patent No. 5892017
 GENERAL INFORMATION:

APPLICANT: Lee, James
 TITLE OF INVENTION: NUCLEIC ACID ENCODING PFAA RECEPTOR
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/802,627A
 FILING DATE: 19-Feb-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/284586
 FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA: 08/076093
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P0706P2P1D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-802-627A-4

LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-802-627A-4

Query Match 45.0%; Score 49; DB 2; Length 352;
 Best Local Similarity 47.1%; Pred. No. 25;
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17
 DB 47 IIFLTGIVNGLVILWM 63

RESULT 11
 US-08-801-238-4
 Sequence 4, Application US/08801238
 Patent No. 5919896
 GENERAL INFORMATION:

APPLICANT: Lee, James
 TITLE OF INVENTION: PFAA RECEPTOR
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/801,238
 FILING DATE: 19-Feb-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/284586
 FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA: 08/076093
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/810782
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P0706P2P1D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-801-238-4

LENGTH: 352 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-801-238-4

Query Match 45.0%; Score 49; DB 2; Length 352;
 Best Local Similarity 47.1%; Pred. No. 25;
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17
 DB 47 IIFLTGIVNGLVILWM 63

RESULT 12

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US-08-801-228-4
: Sequence 4, Application US/08801228
: Patent No. 5922541
: GENERAL INFORMATION:
: APPLICANT: Lee, James
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
: TITLE OF INVENTION: PFA4 RECEPTOR NUCLEIC ACID
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/801,228
: FILING DATE: 19-Feb-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/284586
: FILING DATE: 10-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/076093
: FILING DATE: 11-JUN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/810782
: FILING DATE: 19-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P0706P2PID3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-5530
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 352 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
: US-08-801-228-4
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: Query Match 45.0%; Score 49; DB 2; Length 352;
: Best Local Similarity 47.1%; Pred. No. 25;
: Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
:
: Cy 1 IIILSLIGGGLIIII 17
: Db 47 IIFLGIIVGNGLVIIIVM 63
:
: RESULT 13
: US-09-104-296-4
: Sequence 4, Application US/09104296
: Patent No. 6087475
: GENERAL INFORMATION:
: APPLICANT: Lee, James
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: PFA4 Receptors
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA

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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,296
FILING DATE: 24-June-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/701265
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/664228
FILING DATE: 06-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-104-296-4

Query Match 45.0%; Score 49; DB 3; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IILITSLGGGLILIT 17
Db 47 IILITSLGGGLILIT 63

RESULT 14
US-09-517-605-4
Sequence 4, Application US/09517605
Patent No. 6391567
GENERAL INFORMATION:
APPLICANT: Lileman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Gelberbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-517-605-4

Query Match 45.0%; Score 49; DB 4; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Oy 1 IILITSLGGGLILIT 17

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Db 47 IIFLTGIVGNGLVILVM 63

RESULT 15

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US-08-118-270-346
Sequence 346, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-346

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Query Match	44.0%;	Score 48;	DB 1;	Length 94;
Best Local Similarity	27.3%;	Pred. No. 8.4;		
Matches	6;	Conservative	10;	Mismatches 6;
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Db      8 VIIINTIGNILVIMAVCTFY 29
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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1002.770 Million cell updates/sec

Title: US-09-892-949-2_COPY_520_543
Perfect score: 109
Sequence: 1 ILLITSLIGGGLIILLITVAYGL 24

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Total number of hits satisfying chosen parameters: 492763

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	649	11	US-09-892-949-46
2	109	100.0	652	11	US-09-972-708-14
3	109	100.0	652	15	US-10-006-265-2
4	109	100.0	662	11	US-09-972-708-15
5	109	100.0	662	11	US-09-892-949-54
6	109	100.0	662	15	US-10-006-265-17
7	109	100.0	732	11	US-09-892-949-2
8	109	100.0	745	11	US-09-972-708-4
9	83	75.1	662	11	US-09-892-949-57
10	82	75.2	726	11	US-09-972-708-12
11	57	52.3	463	15	US-10-156-761-8893
12	51	46.8	175	15	US-10-156-761-13642
13	51	46.8	302	12	US-10-017-161-1052
14	51	46.8	318	10	US-09-886-055-273
15	51	46.8	318	11	US-09-804-291-273

16	49.5	45.4	363	10	US-09-738-626-5615	Sequence 5615, App
17	49	45.0	270	12	US-10-017-161-856	Sequence 856, App
18	49	45.0	352	10	US-09-953-692-2	Sequence 2, Appl1
19	49	45.0	352	10	US-09-953-717-2	Sequence 2, Appl1
20	49	45.0	352	10	US-09-104-063-4	Sequence 4, Appl1
21	49	45.0	352	10	US-09-870-759-37	Sequence 37, Appl1
22	49	45.0	352	10	US-09-870-759-144	Sequence 144, Appl1
23	49	45.0	352	12	US-10-251-703-18	Sequence 38, Appl1
24	49	45.0	352	15	US-10-225-567A-76	Sequence 76, Appl1
25	49	45.0	352	15	US-10-245-850-1	Sequence 1, Appl1
26	49	45.0	397	10	US-09-712-363-280	Sequence 280, App
27	48	44.0	18	15	US-10-084-813-127	Sequence 127, App
28	47	43.1	24	12	US-10-251-703-39	Sequence 39, Appl1
29	47	43.1	36	11	US-09-983-802-197	Sequence 197, App
30	47	43.1	272	9	US-09-755-456-10	Sequence 10, Appl1
31	47	43.1	299	10	US-09-886-055-41	Sequence 41, Appl1
32	47	43.1	299	11	US-09-804-291-41	Sequence 41, Appl1
33	47	43.1	299	12	US-10-017-161-232	Sequence 232, App
34	46.5	42.7	109	11	US-09-764-891-4763	Sequence 4763, App
35	46.5	42.7	109	15	US-10-091-572-318	Sequence 318, App
36	46.5	42.7	192	11	US-09-776-724A-110	Sequence 110, App
37	46	42.2	78	9	US-09-864-761-37650	Sequence 37650, App
38	46	42.2	93	9	US-09-811-284-250	Sequence 250, App
39	46	42.2	158	10	US-09-747-155-218	Sequence 218, App
40	46	42.2	275	9	US-09-755-456-9	Sequence 9, Appl1
41	46	42.2	277	9	US-09-755-456-7	Sequence 7, Appl1
42	46	42.2	293	12	US-10-017-161-818	Sequence 818, App
43	46	42.2	321	9	US-09-815-242-4890	Sequence 4890, App
44	46	42.2	321	9	US-09-815-242-10635	Sequence 10635, App
45	46	42.2	355	15	US-10-237-563-30	Sequence 30, Appl1

ALIGNMENTS

RESULT 1
US-09-892-949-46
; Sequence 46, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-46
Query Match 100.0%; Score 109, DB 11;
Best Local Similarity 100.0%; Pred. No. 9.56-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ILLITSLIGGGLIILLITVAYGL 24
DB 520 ILLITSLIGGGLIILLITVAYGL 543

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RESULT 2
US-09-972-708-14
; Sequence 14, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Cosman, David J.
; APPLICANT: Bird, Timothy A.
; APPLICANT: DuBoise, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-14

Query Match      100.0%; Score 109; DB 11; Length 652;
Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      533 ILLITSLIGGGLILLITLVAYGL 556

RESULT 3
US-10-006-265-2
; Sequence 2, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: JP 11/217797
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-2

Query Match      100.0%; Score 109; DB 15; Length 652;
Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      533 ILLITSLIGGGLILLITLVAYGL 556

RESULT 4
US-09-972-708-15
; Sequence 15, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
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; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: DuBoise, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-15

Query Match      100.0%; Score 109; DB 11; Length 662;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILLITSLIGGGLILLITLVAYGL 24
Db      533 ILLITSLIGGGLILLITLVAYGL 556

RESULT 5
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; Sequence 54, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Candy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-54

Query Match      100.0%; Score 109; DB 11; Length 662;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ILLITSLIGGGLILLITLVAYGL 24
Db      533 ILLITSLIGGGLILLITLVAYGL 556

RESULT 6
US-10-006-265-17
; Sequence 17, Application US/10006265
; Publication No. US20030125520A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030125520A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
; FILE REFERENCE: 06501-096001
; CURRENT APPLICATION NUMBER: US/10/006,265
```



```
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/JP00/03556
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: JP 11/155797
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: JP 11/217797
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-265-17

Query Match          100.0%; Score 109; DB 15; Length 662;
Best Local Similarity 100.0%; Pred. No. 9,7e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITLVAYGL 24
Db 533 IILITSLIGGGLIILITLVAYGL 556

RESULT 7
US-09-892-949-2
; Sequence 2, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 732
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-2

Query Match          100.0%; Score 109; DB 11; Length 732;
Best Local Similarity 100.0%; Pred. No. 1,1e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITLVAYGL 24
Db 520 IILITSLIGGGLIILITLVAYGL 543

RESULT 8
US-09-972-708-4
; Sequence 4, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
```

```
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-4

Query Match          100.0%; Score 109; DB 11; Length 745;
Best Local Similarity 100.0%; Pred. No. 1,1e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITLVAYGL 24
Db 533 IILITSLIGGGLIILITLVAYGL 556

RESULT 9
US-09-892-949-57
; Sequence 57, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 662
; TYPE: PRT
; ORGANISM: mus musculus
US-09-892-949-57

Query Match          76.1%; Score 83; DB 11; Length 662;
Best Local Similarity 66.7%; Pred. No. 0.0029;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILITLVAYGL 24
Db 534 IILITSLIGGGLIILITLVAYGL 557

RESULT 10
US-09-972-708-12
; Sequence 12, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
```

```

; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 726
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-972-708-12

```

Query Match	75.2%	Score 82	DB 11	Length 726
Best Local Similarity	62.5%	Pred. No. 0.0043		
Matches 15, Conservative	6	Mismatches 3	Indels 0	Gaps 0

```

QY      1 IILITSLIGGGLLILITVAYGL 24
          :::|::|::|::|::|::|::|::|
Db      517 VVLLTSLVGGGLLSIKVTFFGL 540

```

```

RESULT 11
US-10-156-761-8893
Sequence 8893, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHITAKA
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8893
LENGTH: 463
TYPE: PAT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8893

```

Query Match	52.3%	Score 57	DB 15	length 463
Best Local Similarity	55.6%	Pred. No. 5.7		
Matches 10, Conservative		5, Mismatches 3	Indels 0	Gaps 0

```
QY      2 ILTSLIGGGLLILIT 19
        ||:|:|||||: :|: |
Db     235 ILTALIGGGLFVLVAYT 252
```

RESULT 12
US-10-156-761-13642
Sequence 13642, Application US/10156761
Publication NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-1262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697

```

; PRIOR FILING DATE: 2001-08-02
;
; NUMBER OF SEQ ID NOS: 15109
;
; SEQ ID NO 13642
;
; LENGTH: 175
;
; TYPE: PRT
;
; ORGANISM: Streptomyces avermitilis
;
US-10-156-761-13642

```

Query Match	46.8%	DB 15;	Length 175;
Best Local Similarity	42.9%	Score. No. 13;	
Matches	9;	Conservative	7;
		Mismatches	5;
		Indels	0;
		Gaps	0;

```
QY      1 ILITSLIGGGLILILITVA 21
      ::|: |||||: ||:| |
Db     38 VLLVLLLGGLIGLVLSA 58
```

```

RESULT 13
US-10-017-161-1052
Sequence 1052, Application US/10017161
Publication No. US20030143686A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIHO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKITAMA, YUTAKA
APPLICANT: ABUTATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 08435/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1052
LENGTH: 302
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-161-1052

```

Query Match	46.8%	Score 51	DB 12	Length 302
Best Local Similarity	57.9%	Pred. NO. 23		
Matches 11, Conservative	3	Mismatches 5	Indels 0	Gaps 0

```
QY      1 IILTSLIGGGLLIILT 19
        | :|:| | | | |
Db      35 ISYVTALLGNSLLFIILT 53
```

```

RESULT 14
US-09-886-055-273
Sequence 273, Application US/09886055
Patent No. US2002013273A1
GENERAL INFORMATION:
APPLICANT: STRYER, LUBERT
APPLICANT: ZOZULYA, SERGEY
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
FILE REFERENCE: 078003-0277150
CURRENT APPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
NUMBER OF SEQ ID NOS: 522
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 273
LENGTH: 318
TYPE: prt
ORGANISM: Homo sapiens
US-09-886-055-273

```

Query Match	46.8%;	Score 51;	DB 10;	length 318;
Best Local Similarity	57.9%;	Pred. No. 24;		

Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 IILITSLIGGGLIILIT 19
 | : | : | | | | |
 Db 35 ISYVTALGNSLIIFILIT 53

RESULT 15
 US-09-804-291-273
 ; Sequence 273, Application US/09804291
 ; Publication No. US20030088059A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZOZULA, SERGEY
 ; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
 ; FILE REFERENCE: P 0278005
 ; CURRENT FILING DATE: 2001-03-13
 ; PRIOR APPLICATION NUMBER: US/09/804,291
 ; PRIOR FILING DATE: 2000-03-13
 ; PRIOR APPLICATION NUMBER: 60/188,914
 ; PRIOR FILING DATE: 2000-03-13
 ; PRIOR APPLICATION NUMBER: 60/192,033
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: 60/198,474
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/199,335
 ; PRIOR FILING DATE: 2000-04-24
 ; PRIOR APPLICATION NUMBER: 60/207,702
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/213,849
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/226,534
 ; PRIOR FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: 60/230,732
 ; PRIOR FILING DATE: 2000-09-07
 ; PRIOR APPLICATION NUMBER: 60/266,862
 ; PRIOR FILING DATE: 2001-02-07
 ; NUMBER OF SEQ ID NOS: 529
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 273
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-804-291-273

Query Match 46.8%; Score 51; DB 11; Length 318;
 Best Local Similarity 57.9%; Pred. No. 24;
 Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLIILIT 19
 | : | : | | | | |
 Db 35 ISYVTALGNSLIIFILIT 53

Search completed: August 18, 2003, 13:33:24
 Job time : 4.46873 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 18, 2003, 13:23:02 ; Search time 3.36342 Seconds
(without alignments)
686.221 Million cell updates/sec

Title: US-09-892-949-2_COPY_520_543
Perfect score: 109
Sequence: 1 ILLITSLIGGGLLILITLVAYGL 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	50.5	662	2 A54078	methyl-accepting c
2	52	47.7	527	2 H72536	probable oligopept
3	51	46.8	97	2 C75415	hypothetical prote
4	51	46.8	206	2 T34961	probable membrane
5	51	46.8	280	1 C70784	probable dihem c
6	51	46.8	329	2 H64220	membrane protein m
7	51	46.8	465	2 H87591	sensor histidine k
8	51	46.8	530	2 E82189	methyl-accepting c
9	50.5	46.3	580	2 S76846	hypothetical prote
10	50.5	46.3	1433	1 GNVBDM	M polypeptide prec
11	50	45.9	366	2 G00048	catonic amino aci
12	49	45.0	352	2 G00048	fusin (BESTRA) - c
13	49	45.0	352	2 G00048	neuropeptide Y/pep
14	49	45.0	353	2 S28787	conserved hypochet
15	49	45.0	353	2 H75265	histidine kinase-1
16	49	45.0	360	2 E95273	probable serine pr
17	49	45.0	368	2 A96929	hypothetical prote
18	49	45.0	397	2 H70789	hypothetical prote
19	49	45.0	413	2 T23766	hypothetical prote
20	49	45.0	455	2 A75121	hypothetical prote
21	49	45.0	539	2 T27559	hypothetical prote
22	49	45.0	929	2 T32492	hypothetical prote
23	49	44.5	1124	2 B84742	probable receptor
24	48.5	44.5	266	2 AB2270	hypothetical prote
25	48	44.0	339	2 D83201	probable glycosyl
26	48	44.0	397	2 T44477	hypothetical prote
27	48	44.0	401	2 F87196	probable membrane
28	48	44.0	405	2 H83798	ABC transporter (p
29	48	44.0	432	2 T21880	hypothetical prote

30	48	44.0	505	2 B88206	protein F21D12.3 [
31	47.5	43.6	398	2 B71193	hypothetical prote
32	47.5	43.6	448	2 F82280	citrate/sodium sym
33	47	43.1	322	2 A64023	hypothetical prote
34	47	43.1	343	2 AD1502	hypothetical prote
35	47	43.1	423	2 T26306	hypothetical prote
36	47	43.1	430	2 F70016	purine permease ho
37	47	43.1	473	2 AF1207	ABC transporters (
38	47	43.1	662	2 D54078	methyl-accepting c
39	46.5	42.7	446	2 A38244	citrate transport
40	46	42.2	96	2 E69790	hypothetical prote
41	46	42.2	153	2 T17893	hypothetical prote
42	46	42.2	202	2 JC4635	tumor-associated l
43	46	42.2	202	2 JC6205	cell surface anti
44	46	42.2	216	2 H83757	hypothetical prote
45	46	42.2	242	2 A69026	conserved hypothet

ALIGNMENTS

RESULT 1

A54078 methyl-accepting chemotaxis protein mcpB - Bacillus subtilis

C/Species: Bacillus subtilis
C/Date: 06-Jan-1995 #sequence #revision 06-Jan-1995 #text_change 20-Jun-2000

C/Accession: A54078; H69655

R/Hanlon, D.W., Ordal, G.W.
J. Biol. Chem. 269, 14038-14046, 1994

A/Title: Cloning and characterization of genes encoding methyl-accepting chemotaxis prot

A/Reference number: A54078; MUID:94245722; PMID:818684

A/Accession: A54078

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-662 <HAN>

A/Cross-References: GB:L29189; NID:9459687

A/Note: The sequence in GenBank entry BACMCPBP, release 106.0. (PID:9459688) has 360-N

R/Kunze, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berier

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chic

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Ertter, C.; Ferrati, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier

leoh, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koester, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maesuda, S.; Mauesl

Y, M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, W.; Sadate, Y.; Sato, T.; Scanlon,

A/Authors: Schlach, S.; Schroeter, R.; Scifone, F.; Sekiguchi, J.; Sekowska, A.; Seto

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, f

A/Authors: Yoshikawa, H.F.; Zumberstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: H69655

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-359 'N', 361-449 'G', 451-662 <KUN>

A/Cross-References: GB:Z99119; GB:Z99120; GB:AL009126; NID:92635613; PIDN:CAB15115.1; PI

A/Experimental source: strain 168

C/Comment: Strains in which this protein is inactivated are defective in chemotaxis towz

C/Genetic: C;Gene: mcpB

A/Superfamily: probable methyl-accepting chemotaxis transducer

C/Keywords: chemotaxis; signal transduction; transmembrane protein

Query Match 50.5%; Score 55; DB 2; Length 662;

Best Local Similarity 55.6%; Pred. No. 11;

Matches 10; Conservativity 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILLITSLIGGGLLILITL 18

DB 286 IVLINSLVAGLILITLV 303

A/Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
A/Reference number: A64300; MUID:96337999; PMID:868087
A/Accession: C64449
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-366 <BUL>
A/Cross-references: GB:U67561; GB:L77117; NID:92826373; PIDN:AA99200.1; PID:91591825; T
C/Genetics:
A/Map position: REV1140149-1139049
C/Superfamily: probable cationic amino acid transporter MCAT-2

Query Match 45.0%; Score 50; DB 2; Length 366;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 ILITSLIGGGLILIT 19
DB 12 LITSLVGGGIFVLSPLT 29

RESULT 12

G00048
fusin (LESTRA) - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999
C/Accession: G00048
R/Tatsumi, M.
Submitted to GenBank, July 1996
A/Reference number: H00048
A/Accession: G00048
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-352 <TRT>
A/Cross-references: GB:D86579; NID:91468948; PID:91468948
C/Superfamily: vertebrate rhodopsin

Query Match 45.0%; Score 49; DB 2; Length 352;
Best Local Similarity 47.1%; Pred. No. 37;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILIT 17
DB 47 IIFLTGIVGNGLVILWM 63

RESULT 13

A45747
neuropeptide Y/peptide YY receptor Y3 - human
N/Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; re
C/Species: Homo sapiens (man)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C/Accession: A45747; A53103; I53006; I59444; I59203; S32761
R/Federapfel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis
Genomics 16, 707-712, 1993
A/Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu
A/Reference number: A45747; MUID:93315164; PMID:8325644
A/Accession: A45747

A/Molecule type: mRNA
A/Residues: 1-352 <RED>
A/Cross-references: GB:W92993; NID:9292516; PIDN:AAA16617.1; PID:9292517
R/Loebercher, M.; Geisler, T.; O'Reilly, T.; Zwaalen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A/Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly e
A/Reference number: A53103; MUID:94103215; PMID:8276799
A/Accession: A53103

A/Molecule type: mRNA
A/Residues: 1-352 <LOB>
A/Cross-references: EMBL:X71635; NID:9297099; PIDN:CAA50641.1; PID:9297100
R/Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A/Title: Molecular cloning, characterization, and localization of the human homolog to c
A/Reference number: I53006; MUID:93319629; PMID:8329116
A/Accession: I53006

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-352 <HER>

A/Cross-references: GB:U67561; NID:9414929; PIDN:AAA03209.1; PID:9414928
R/Jazini, E.B.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lar
Regul. Pept. 47, 247-258, 1993
A/Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolo
A/Reference number: I59444; MUID:94052833; PMID:8234909
A/Accession: I59444

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-352 <RE2>

A/Cross-references: GB:L01639; NID:9189313; PIDN:AAA16594.1; PID:9189314
R/Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993

A/Title: Molecular cloning of cDNAs encoding a L078 receptor and putative leukocyte chem

A/Reference number: I54751; MUID:94092629; PMID:7505609
A/Accession: I69203

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-352 <RES>

A/Cross-references: GB:D10924; NID:9219868; PIDN:BA01722.1; PID:9219869

C/Genetics:

A/Gene: GDB:NPYR, NPYX3

A/Cross-references: GDB:230002; OMIM:162643

A/Map position: 2q21-2q21

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 45.0%; Score 49; DB 2; Length 352;
Best Local Similarity 47.1%; Pred. No. 37;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILIT 17
DB 47 IIFLTGIVGNGLVILWM 63

RESULT 14

S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C/Accession: S28787
R/Rimland, J.; Xin, W.; Sweetnam, P.; Saljoh, K.; Neetler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A/Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A/Reference number: S28787; MUID:92100053; PMID:1661837
A/Accession: S28787

A/Molecule type: mRNA

A/Residues: 1-353 <RIM>

A/Cross-references: EMBL:M86739

C/Superfamily: vertebrate rhodopsin

C/Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 45.0%; Score 49; DB 2; Length 353;
Best Local Similarity 47.1%; Pred. No. 37;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLILIT 17
DB 48 IIFLTGIVGNGLVILWM 64

RESULT 15

H75265
conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)
C/Species: *Deinococcus radiodurans*
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C/Accession: H75265
R/White, O.; Eilen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanatkevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Mc
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; M0ID:20036896; PMID:10567266
 A/Accession: H75265
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1353 <WHI>
 A/Cross-references: GB:AE002080; GB:AE000513; NID:g6460327; PIDN:AAF12054.1; PID:g646033
 A/Experimental source: strain R1
 C/Genetics:
 A/Gene: DR2513
 A/Map position: 1

Query Match 45.0%; Score 49; DB 2; Length 353;
 Best Local Similarity 42.9%; Pred. No. 37;
 Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 2 ILTSLIGGGLLILITVAY 22
 :|::|||::|:|:
 Db 268 VILSTRGGSLTYLLITLAY 288

Search completed: August 18, 2003, 13:31:24
 Job time : 5.36342 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:27 ; Search time 1.82423 Seconds.

(without alignments)
618,695 Million cell updates/sec

Title: US-09-892-949-2_COPY_520_543
Perfect score: 109
Sequence: 1 IILITSLIGGGLIILITVAVGL 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	50.5	662	1 MCPB_BACSU	P39215 bacillus su
2	51	46.8	280	1 QCRG_MYCTU	Q10386 mycobacteri
3	51	46.8	339	1 Y188_MYCGE	P47434 mycoplasma
4	50.5	46.3	1433	1 VGLM_BUNYM	P04505 bunyamwera
5	49	45.0	192	1 CCR4_SHEEP	Q28553 ovine aries
6	49	45.0	349	1 CCR4_RAT	Q08565 ratius norv
7	49	45.0	352	1 CCR4_CERTO	Q62747 cercocebus
8	49	45.0	352	1 CCR4_HUMAN	P30991 homo sapien
9	49	45.0	352	1 CCR4_MACFA	Q28474 macaca fasc
10	49	45.0	352	1 CCR4_PAPAN	P79394 macaca mula
11	49	45.0	353	1 CCR4_PAPAN	P56491 papio anubi
12	49	45.0	353	1 CCR4_BOVIN	P25930 bos taurus
13	49	45.0	353	1 CCR4_FELICA	P56498 felis silve
14	49	45.0	359	1 CCR4_MOUSE	P70658 m-c-x-che
15	47	43.1	430	1 YC48_HABIN	P44336 haemophilus
16	47	43.1	432	1 PUCK_BACSU	Q32140 bacillus su
17	47	43.1	662	1 TLBP_BACSU	P39217 bacillus su
18	46.5	42.7	446	1 CITN_KLEPN	P31602 klebsiella
19	46	42.2	202	1 T4S1_MESAU	P49111 mesocricetu
20	46	42.2	283	1 YD03_SCHPO	Q10327 schizosacch
21	46	42.2	291	1 Y4TQ_RHISN	Q51392 rhizobium s
22	46	42.2	321	1 MRAY_ENTFA	Q07107 enterococcu
23	46	42.2	353	1 ILBB_GORGO	Q28422 gorilla gor
24	45	41.3	144	1 YL05_METUA	Q60304 methanococc
25	45	41.3	347	1 CDD2_HORSE	P37998 equus cabal
26	45	41.3	370	1 GP10_RAT	Q64121 ratius norv
27	45	41.3	518	1 C317_DROME	Q94776 drosophila
28	45	41.3	553	1 GP11_CANAL	Q74248 candida alb
29	45	41.3	557	1 UBIB_XANAC	Q8PQ00 xanthomonas
30	45	41.3	571	1 UBIB_XANCP	Q8PQ01 xanthomonas
31	44.5	40.8	379	1 CIT2_ECOLI	P05883 escherichia
32	44.5	40.8	481	1 YWBL_BACSU	P39595 bacillus su
33	44	40.4	170	1 HEMK_PROMI	Q51887 proteus mir

34	44	40.4	202	1 T4S1_HUMAN	P30408 homo sapien
35	44	40.4	285	1 FOCA_ECOLI	P21501 escherichia
36	44	40.4	370	1 GP10_HUMAN	P49683 homo sapien
37	44	40.4	435	1 A2AR_CARAU	P32251 carassius a
38	44	40.4	438	1 PEUX_BACSU	P42086 bacillus su
39	44	40.4	460	1 NU4M_BRARE	Q9mly1 brachydanio
40	44	40.4	460	1 NU4M_CARAU	Q78687 carassius a
41	44	40.4	460	1 NU4M_CROLA	P34194 crossostoma
42	44	40.4	460	1 NU4M_ONCMY	P11631 oncorhynchus
43	44	40.4	460	1 NU4M_SALSA	Q9zzm4 salmo salar
44	44	40.4	659	1 Y102_MYCLE	P53525 mycobacteri
45	44	40.4	764	1 CP11_MOUSE	P97742 mus musculu

ALIGNMENTS

RESULT 1
MCPB_BACSU
ID MCPB_BACSU STANDARD; PRT; 662 AA.
AC P39215;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methy1-accepting chemotaxis protein mcpb (H3).
OS MCPB.
NCBI Taxid=1423;
NCBI Taxid=1423;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=168 / O11085;
RX MEDLINE=94245722; PubMed=8188684;
RT Hanlon D.W., Ordal G.W.;
RT "Cloning and characterization of genes encoding methy1-accepting
RT chemotaxis proteins in Bacillus subtilis.";
RT J. Biol. Chem. 269:14038-14046(1994).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunze F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Broutillet S., Brunsch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani U.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holseppel S., Hosono S., Hullo M.F., Iraya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarovic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maul C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prescan E., Puig C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scofield F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Taniyama S., Tognoni A.,
RA Toseno V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wamput R., Wedler E., Wedler H., Wellzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumslein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -!- FUNCTION: RESPONSIBLE FOR DETECTING A SUBSET OF AMINO ACIDS THAT

CC INCLUDES ASPARAGINE, ASPARTATE, GLUTAMINE, AND HISTIDINE.
CC -1- FUNCTION: CHEMOTACTIC-SIGNAL TRANSDUCERS RESPOND TO CHANGES IN THE
CC CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT,
CC TRANSDUCE A SIGNAL FROM THE OUTSIDE TO THE INSIDE OF THE CELL, AND
CC FACILITATE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL
CC OF METHYLATION. ALL AMINO ACIDS SERVE AS ATTRACTANTS IN
CC B. SUBTILIS, THEY APPEAR TO CAUSE AN INCREASE IN THE TURNOVER
CC METHYL GROUPS, LEADING TO METHYLATION OF AN UNIDENTIFIED ACCEPTOR,
CC WHILE REPELLENTS HAVE BEEN SHOWN TO CAUSE A DECREASE IN METHYL
CC GROUP TURNOVER. THE METHYL GROUPS ARE ADDED BY A METHYLTRANSFERASE
CC AND REMOVED BY A METHYLESTERASE.
CC -1- SIMILARITY: Contains 1 methyl-accepting transducer domain.
CC -1- SIMILARITY: Contains 1 HAMM domain.
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DR EMBL; L29189; AAA20554.1; -;
DR EMBL; Z99119; CAB15104.1; -;
DR EMBL; Z99120; CAB15115.1; -;
DR PIR; A54078; A54078.
DR HSSP; P02942; 10U7.
DR Subtilisin; BG10859; mcpB.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR004089; Chmexis_transd.
DR InterPro; IPR003660; HAMM.
DR InterPro; IPR003122; TarH.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00672; HAMM; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR Pfam; PF02203; TarH; 1.
DR SMART; SM00304; HAMM; 1.
DR SMART; SM00283; MA; 1.
DR SMART; SM00319; TarH; 1.
DR PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
DR PROSITE; PS50885; HAMM; 1.
KW Chemotaxis; Transducer; Transmembrane; Methylation; Complete proteome.
CC
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1 37 POTENTIAL.
FT DOMAIN 38 282 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 283 303 POTENTIAL.
FT DOMAIN 304 662 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 304 356 HAMM.
FT DOMAIN 375 611 METHYL-ACCEPTING TRANSDUCER.
FT MOD_RES 371 371 DEAMIDATION AND METHYLATION
FT MOD_RES 371 371 DEAMIDATION AND METHYLATION
FT MOD_RES 595 595 (BY SIMILARITY).
FT MOD_RES 630 630 METHYLATION (BY SIMILARITY).
FT MOD_RES 637 637 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 662 AA; 71885 MW; 98DD181PB4690BC CRC64;
Query Match 50.5%; Score 55; DB 1; Length 662;
Best Local Similarity 55.6%; Pred. No. 7.2;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Db 1 ILLITSLIGGLILITL 18
286 IVLASIVAGLILITIV 303
RESULT 2
QCRC MYCTU STANDARD; PRT; 280 AA.
ID QCRC MYCTU
AC Q10366;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ubiquinol-cytochrome C reductase cytochrome C subunit.
GN QCRC OR RV2194 OR MT2250 OR MTCY150.05.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1773;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigler R., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Ruster S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulten J.E., Taylor K., Whitehead S., Barrett B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF THE UBIQUINOL-CYTOCHROME C COMPLEX
CC ARE: CYTOCHROME B, THE RIBOSE PROTEIN AND A CYTOCHROME C SUBUNIT.
CC -1- SIMILARITY: SOME, TO CYTOCHROME C.

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DR EMBL; Z70283; CAA94263.1; -;
DR EMBL; AB007071; AAK46536.1; -;
DR PIR; C70784; C70784.
DR TIGR; MT250; -;
DR Tuberculin; RV2194; -;
DR InterPro; IPR003088; Cyt C1.
DR InterPro; IPR000345; CytC_heme_bind.
DR Pfam; PF00034; cytochrome_c; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 2.
KW Electron transport; Heme; Transmembrane; Complete proteome.
FT BINDING 73 73 HEME 1 (COVALENT) (POTENTIAL).
FT BINDING 76 76 HEME 1 (COVALENT) (POTENTIAL).
FT METAL 77 77 IRON (HEME 1 AXIAL LIGAND) (POTENTIAL).
FT BINDING 174 174 HEME 2 (COVALENT) (POTENTIAL).
FT BINDING 177 177 HEME 2 (COVALENT) (POTENTIAL).
FT METAL 178 178 IRON (HEME 2 AXIAL LIGAND) (POTENTIAL).
FT TRANSSEM 25 45 POTENTIAL.
FT TRANSSEM 258 278 POTENTIAL.
SQ SEQUENCE 280 AA; 29138 MW; 7A058AE7E12BF713 CRC64;
Query Match 46.8%; Score 51; DB 1; Length 280;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Db 8 IGGGLILITLVAYGL 24
25 LSGVLLTALTITAGGL 41

RESULT 3
 ID Y188 MYCGE STANDARD; PRT; 329 AA.
 AC P47434;
 RN 11;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable ABC transporter permease protein MG188.
 GN MG188.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NC NCBI_TaxID=2097;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=96026346; PubMed=7569993;
 RA Frazer C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
 RA Nguyen D.T., Utechtack T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bort K.F., Hu P.-C., Lucier T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RL Science 270:337-403(1995).
 CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
 CC SUBSTRATE ACROSS THE MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM PERMEASE FAMILY. MALRG SUBFAMILY.
 CC -----
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 CC -----
 CC DR EMBL; U39698; AAC71407.1; -
 CC DR PIR; H64220; H64220.
 CC DR TIGR; MG188; -
 CC DR InterPro; IPR000515; BPD transp.
 CC DR Pfam; PF00528; BPD transp; 1.
 CC DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; FALSE NEG.
 CC KM Hypothetical protein: Transport; Transmembrane; Complete proteome.
 CC FT TRANSMEM 30 50 POTENTIAL.
 CC FT TRANSMEM 96 116 POTENTIAL.
 CC FT TRANSMEM 128 148 POTENTIAL.
 CC FT TRANSMEM 176 196 POTENTIAL.
 CC FT TRANSMEM 234 254 POTENTIAL.
 CC FT TRANSMEM 283 303 POTENTIAL.
 CC SQ SEQUENCE 329 AA; 37201 MW; 45BFB75ACBBA25 CRC64;
 Query Match 46.8%; Score 51; DB 1; Length 329;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 5 TSLIGGGLILILITVAYGL 24
 DB 282 TNLGATVTLVFLVGVCYGL 301
 RESULT 4
 VGLM_BUNYW STANDARD; PRT; 1433 AA.
 AC P04505;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE M polypeptide precursor [contains: Glycoprotein G2; Nonstructural
 DE protein NS-M; Glycoprotein G1].
 GN M.

OS Bunyamwera virus.
 OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.
 NC NCBI_TaxID=11573;
 RN 11;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86098655; PubMed=3753629;
 RA Lees J.F., Pringle C.R., Elliott R.M.,
 RT "Nucleotide sequence of the Bunyamwera virus M RNA segment:
 RT conservation of structural features in the Bunyavirus glycoprotein
 RT gene product";
 RL Virology 148:1-14(1986).
 CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
 CC INCLUDING NONSTRUCTURAL PROTEIN NS-M, GLYCOPROTEIN G1, AND
 CC GLYCOPROTEIN G2.
 CC -1- SIMILARITY: BELONGS TO THE BUNYAVIRUSES M POLYPROTEIN FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; M1852; AAA42777.1; -
 CC DR PIR; A04101; GNVBW.
 CC DR InterPro; IPR005167; Bunya G1.
 CC DR InterPro; IPR005168; Bunya G2.
 CC DR Pfam; PF03557; Bunya_G1; 1.
 CC DR Pfam; PF03563; Bunya_G2; 1.
 CC KM Polypeptide; Glycoprotein; Transmembrane; Nonstructural protein;
 CC signal.
 CC FT SIGNAL 1 16
 CC FT CHAIN 17 1433 M POLYPROTEIN.
 CC FT CHAIN 17 302 GLYCOPROTEIN G2.
 CC FT CHAIN 303 477 NONSTRUCTURAL PROTEIN NS-M.
 CC FT CHAIN 478 1433 GLYCOPROTEIN G1.
 CC FT TRANSMEM 1382 1409 POTENTIAL.
 CC FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 1169 1169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 1433 AA; 162077 MW; CD61ABDE782018E0 CRC64;
 Query Match 46.3%; Score 50.5; DB 1; Length 1433;
 Best Local Similarity 62.5%; Pred. No. 49;
 Matches 15; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
 QY 1 IILITSLGGGLILILITVAYGL 24
 DB 364 IILYTSLEFAGLTI-IPAGVNLGL 386
 RESULT 5
 CCR4_SHEEP STANDARD; PRT; 192 AA.
 AC Q28553;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)
 DE (Stromal cell-derived factor 1 receptor) (Fusin) (Leukocyte-derived
 DE seven transmembrane domain receptor) (LSTR) (Fragment).
 GN CXCR4 OR LSTR.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NC NCBI_TaxID=9940;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RA Dyer C.J., Mattern R.L., Kessler D.H.;

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RT      "Development of an ovine Y3 cDNA and expression of the Y3 receptor
RT      RNA in the ovine hypothalamus and pituitary."
RL      Abstr. - Soc. Neurosci. 21:1890-1890(1995).
CC      -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC      SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- PTM: SULFATED (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -1- CAUTION: Was originally (Ref.1) thought to be a receptor for
CC      neuropeptide Y type 3 (NPY3-R).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; U38942; AAA81347.1; -
CC      Interpro; IPR000276; GPCR_Rhodopsn.
CC      Pfam; PF00001; 7tm.1; 1.
CC      DR PRINTS; PR00237; GPCRHOOPS.
CC      DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC      DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
CC      KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC      FT NON_TER 1 1
CC      FT DOMAIN 1 29 1 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 30 53 1 (POTENTIAL).
CC      FT TRANSMEM 54 63 1 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 70 89 2 (POTENTIAL).
CC      FT TRANSMEM 90 100 2 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 101 122 3 (POTENTIAL).
CC      FT TRANSMEM 123 144 3 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 145 165 4 (POTENTIAL).
CC      FT TRANSMEM 166 190 4 (POTENTIAL).
CC      FT TRANSMEM 191 192 5 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 191 192 5 (POTENTIAL).
CC      FT TRANSMEM 191 192 5 BY SIMILARITY.
CC      FT MOD_RES 11 11 SULFATION (POTENTIAL).
CC      FT NON_TER 192 192
CC      FT SEQUENCE 192 AA; 22178 MW; A8BCFE303CS2BD98 CRC64;
CC      -----
Query Match 45.0%; Score 49; DB 1; Length 192;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 IILITSLIGGLILII 17
DB 37 IIFLTGIVNGVLIVM 53

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CC      SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC      INVOLVED IN B-CELL LYMPHOPOIESIS, BONE-MARROW MYELOPOIESIS AND IN
CC      CARDIAC VENTRICULAR SEPTUM FORMATION. PLAYS ALSO AN ESSENTIAL ROLE
CC      IN VASCULARIZATION OF THE GASTROINTESTINAL TRACT, PROBABLY BY
CC      REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN
CC      ENDOTHELIAL CELLS. INVOLVED IN CEREBELLAR NEURONAL LAYER
CC      FORMATION, PREVENTING PREMATURE MIGRATION OF PROLIFERATING GRANULE
CC      CELLS FROM THE EXTERNAL GRANULE LAYER INWARDS. IN THE CNS, COULD
CC      MEDIATE HIPPOCAMPAL-NEURON SURVIVAL (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS AND IN ASTROCYTES.
CC      -1- PTM: SULFATED (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; U90610; AAB50408.1; -
CC      Interpro; IPR000276; GPCR_Rhodopsn.
CC      Pfam; PF00001; 7tm.1; 1.
CC      DR PRINTS; PR00237; GPCRHOOPS.
CC      DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
CC      DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
CC      KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC      FT NON_TER 1 36
CC      FT DOMAIN 1 36 1 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 37 60 1 (POTENTIAL).
CC      FT TRANSMEM 61 76 2 (POTENTIAL).
CC      FT TRANSMEM 77 96 2 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 97 107 3 (POTENTIAL).
CC      FT TRANSMEM 108 129 3 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 130 151 4 (POTENTIAL).
CC      FT TRANSMEM 152 172 4 (POTENTIAL).
CC      FT TRANSMEM 173 197 5 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 198 217 5 (POTENTIAL).
CC      FT TRANSMEM 218 237 6 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 238 258 6 (POTENTIAL).
CC      FT TRANSMEM 259 282 6 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 283 302 7 (POTENTIAL).
CC      FT TRANSMEM 303 349 7 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 349 392 7 BY SIMILARITY.
CC      FT DISULFID 106 183 4 SULFATION (POTENTIAL).
CC      FT MOD_RES 4 4 SULFATION (POTENTIAL).
CC      FT MOD_RES 18 18 N-LINKED (GLCNAC...) (POTENTIAL).
CC      FT CARBOHYD 8 8
CC      FT SEQUENCE 349 AA; 39334 MW; 7E0789A605C60C09 CRC64;
CC      -----
Query Match 45.0%; Score 49; DB 1; Length 349;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 1 IILITSLIGGLILII 17
DB 44 IIFLTGIVNGVLIVM 60

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RESULT 6
CC      CCR4_RAT STANDARD; PRT; 349 AA.
AC 008565;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (stromal cell-
DE derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
DE seven transmembrane domain receptor) (LESTR).
GN CXCR4 OR CXCR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Master; TISSUE=Spleen;
RA Harrison J.K.; Salafina M.N.;
RT "Molecular cloning of rat CXCR4."
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A

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RESULT 7
CC      CCR4_CERTO STANDARD; PRT; 352 AA.
AC 062747;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (stromal cell-
DE derived factor 1 receptor) (Fusin) (LESTR).
GN CXCR4.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Soccy mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.

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OC NCB1_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9831155; PubMed=9656999;
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
 RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys
 naturally infected in west Africa: a comparison of coreceptor usage
 of primary HIV, HIV-2, and SIVmac.";
 RL Virology 246:113-124(1998).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: SUPPRESSED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 or send an email to license@isb.ch).
 CC -----
 DR EMBL, AF051906; AAC39834.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECP_P1.1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECP_P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 39
 FT TRANSMEM 40 63
 FT DOMAIN 64 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 110
 FT TRANSMEM 111 132
 FT DOMAIN 133 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 240
 FT TRANSMEM 241 261
 FT DOMAIN 262 285
 FT TRANSMEM 286 305
 FT DOMAIN 306 352
 FT MOD_RES 21 21
 FT CARBOHYD 11 11
 FT DISULFID 109 186
 SQ SEQUENCE 352 AA; 39648 MW; 4027432B8032F87E CRC64;
 Query Match 45.0%; Score 49; DB 1; Length 352;
 Best Local Similarity 47.1%; Pred. No. 25;
 Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 IILITSLIGGGLILII 17
 Db 47 IIFLTGIVGVILVW 63
 RESULT 8
 CCR4 HUMAN STANDARD; PRT; 352 AA.
 AC P30991; O60835; P56438; O9UKN2;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE C-X-C chemokine receptor type 4 (CXCR-4) (CXCR-4) (stromal cell-
 derived factor 1 receptor) (SDF-1 receptor) (Fusin) (Leukocyte-derived
 seven transmembrane domain receptor) (LESTR) (LCR1) (FB22) (NPYRL)
 DE (HM89) (CD184 antigen).
 GN CXCR4.
 OS Homo sapiens (Human), and
 OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCB1_TaxID=9606, 9598;
 RN [1]-
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human; TISSUE=Lung;
 RX MEDLINE=93319629; PubMed=8329116;
 RA Herzog H., Hott Y.J., Shine J., Selbie L.A.;
 RT "Molecular cloning, characterization, and localization of the human
 homolog to the reported bovine NPY Y3 receptor: lack of NPY binding
 and activation.";
 RL DNA Cell Biol. 12:465-471(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human; TISSUE=Fetal brain;
 RX MEDLINE=94052833; PubMed=8234909;
 RA Jazin E.E., Yoo H., Blomqvist A.G., Yee F., Weng G., Walker M.W.,
 RA Salton J., Lathamar D., Mahlestedt C.R.;
 RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
 human homologue, confers neither NPY binding sites nor NPY
 responsiveness on transfected cells.";
 RL Regul. Pept. 47:247-258(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human; TISSUE=Fetal spleen;
 RX MEDLINE=93315164; PubMed=8235644;
 RA Federspiel B., Melhado I.G., Duncan A.M., Delaney A.D.,
 RA Schappert K.T., Clark-Lewis I., Jirik F.R.;
 RT "Molecular cloning of the cDNA and chromosomal localization of the
 gene for a putative seven-transmembrane segment (7-TMS) receptor
 isolated from human spleen.";
 RL Genomics 16:707-712(1993).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human; TISSUE=Monocytes;
 RX MEDLINE=94103215; PubMed=8276799;
 RA Loetscher M., Gelseer T., O'Reilly T., Zwaalen R., Baggiolini M.,
 RA Moser B.;
 RT "Cloning of a human seven-transmembrane domain receptor, LESTR, that
 is highly expressed in leukocytes.";
 RL J. Biol. Chem. 269:232-237(1994).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human; TISSUE=Monocytes;
 RX MEDLINE=94092629; PubMed=7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a L778 receptor and putative
 leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION OF ITS HIV-1
 RP CORECEPTOR FUNCTION.
 RX MEDLINE=96217947; PubMed=8629022;
 RA Feng Y., Broder C.C., Kennedy P.E., Berger E.A.;
 RT "HIV-1 entry cofactor: functional cDNA cloning of a seven-
 transmembrane, G protein-coupled receptor.";
 RL Science 272:872-877(1996).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human; TISSUE=Peripheral blood leukocytes;
 RX MEDLINE=98136183; PubMed=9468539;
 RA Wegner S.A., Ehrenberg P.K., Chang G., Dayhoff D.E., Sleeker A.L.,
 RA Michel N.L.;
 RT "Genomic organization and functional characterization of the chemokine
 receptor CXCR4, a major entry co-receptor for human immunodeficiency
 virus type 1.";
 RL J. Biol. Chem. 273:4754-4760(1998).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC SPECIES=Human;
 RX MEDLINE=98258970; PubMed=9599023;
 RA Caruz A., Samsom M., Alonso J.M., Alcamí J., Balleux F.,
 RA Virelizier J.L., Parmentier M., Arenzana-Seisdedos F.;

RT "Genomic organization and promoter characterization of human CXCR4
RT gene";
RL FEBS Lett. 426:271-278(1998).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC SPECIES=Human;
RX MEDLINE=99408510; PubMed=10480633;
RA Xiao L., Weiss S.H., Qari S.H., Rudolph D., Zhao C., Denny T.N.,
RA Hodge T., Lai R.B.;
RT "Partial resistance to infection by R5/4 primary HIV type 1 isolates
RT in an exposed-uninfected individual homozygous for CCR5 32-base pair
RT deletion";
RL AIDS Res. Hum. Retroviruses 15:1201-1208(1999).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC SPECIES=Human; TISSUE=Peritoneal blood lymphocytes;
RX MEDLINE=99095114; PubMed=9879064;
RA Froel R., Gierschik P., Moeppe B.;
RT "Genomic organization and expression of the CXCR4 gene in mouse and
RT man: absence of a splice variant corresponding to mouse CXCR4-B in
RT human tissues";
RL J. Recept. Signal Transduct. Res. 18:321-344(1998).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC SPECIES=Human; TISSUE=Neutrophils;
RX MEDLINE=99384048; PubMed=10452968;
RA Gupta S.K., Pillarsetti K.;
RT "CXCR4-Lo: molecular cloning and functional expression of a novel
RT human CXCR4 splice variant";
RL J. Immunol. 163:2368-2372(1999).
RN [12]
RP SEQUENCE FROM N.A.
RC SPECIES=P. troglodytes;
RX MEDLINE=98090115; PubMed=9430250;
RA Pietri J.-L., Zerbib A.C., Girard C., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [13]
RP SULFATION.
RC SPECIES=Human;
RX MEDLINE=99189752; PubMed=10089882;
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
RT entry";
RL Cell 96:667-676(1999).
RN [14]
RP FUNCTION.
RC MEDLINE=96351077; PubMed=8752280;
RA Blasi C.C., Farzan M., Choe H., Parolin C., Clark-Lewis I.,
RA Sodroski J., Springer T.A.;
RT "The lymphocyte chemottractant SDF-1 is a ligand for LESTR/fusin and
RT blocks HIV-1 entry";
RL Nature 382:829-833(1996).
RN [15]
RP FUNCTION.
RC MEDLINE=96351078; PubMed=8752281;
RA Oberlin E., Amara A., Bachelierie F., Beesla C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.P., Loetscher M., Baggiolini M., Moser B.;
RT "The CXC chemokine SDF-1 is the ligand for LESTR/fusin and prevents
RT infection by T-cell-line-adapted HIV-1";
RL Nature 382:833-835(1996).
RN [16]
RP ERRATUM.
RA Oberlin E., Amara A., Bachelierie F., Beesla C., Virelizier J.-L.,
RA Arenzana-Seisdedos F., Schwartz O., Heard J.-M., Clark-Lewis I.,
RA Legler D.P., Loetscher M., Baggiolini M., Moser B.;
RL Nature 384:288-288(1996).
RN [17]
RP CHARACTERIZATION OF ITS HIV-1 CORECEPTOR FUNCTION.
RX MEDLINE=97002453; PubMed=8849450;
RA Lapham C.K., Ouyang J., Chandrasekhar B., Nguyen N.Y., Dimitrov D.S.,

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RA Golding H.;
RT "Evidence for cell-surface association between fusin and the CD4-gp120 complex in human cell lines.";
RL Science 274:602-605(1996).
RN [18]
RX CHARACTERIZATION OF ITS HIV-2 RECEPTOR FUNCTION.
RY MEDLINE=97083584; PubMed=8929542;
RA Endres M.J., Clapham P.R., Marsh M., Ahuja M., Turner J.D.,
RA McHugh A., Thomas J.F., Strobenau-Hagarty B., Choe S., Vance P.J.,
RA Wells T.N.C., Power C.A., Suttenala S.S., Dome R.W., Landau N.R.,
RA Hoxie J.A.;
RT "CD4-independent infection by HIV-2 is mediated by fusin/CXCR4.";
RL Cell 87:745-756(1996).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. INVOLVED IN HAEMATOPOIESIS AND IN CARDIAC VENTRICULAR SEPTUM FORMATION. PLAYS ALSO AN ESSENTIAL ROLE IN VASCULARIZATION OF THE GASTROINTESTINAL TRACT, PROBABLY BY REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN ENDOTHELIAL CELLS. COULD BE INVOLVED IN CEREBELLAR DEVELOPMENT. IN THE CNS, COULD MEDIATE HIPPOCAMPAL-NEURON SURVIVAL. ACTS AS A PRIMARY RECEPTOR FOR SOME HIV-2 ISOLATES AND AS A CO-RECEPTOR WITH CD4 FOR HIV-1 X4 VIRUSES (LYMPHOCTE-TROPIC HIV-1 VIRUSES, ALSO CALLED SYNCYTIUM-INDUCING (SI) STRAINS). PROMOTES ENV-MEDIATED FUSION OF THE VIRUS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P30991-1; Sequence=Displayed;
CC Name=2; Synonyms=CXCR4-I0;
CC IsoId=P30991-2; Sequence=VSP_001890;
CC Note=has been shown to exist only in human so far;
CC -1- TISSUE SPECIFICITY: Expressed in numerous tissues, such as peripheral blood leukocytes, spleen, thymus, spinal cord, heart, placenta, lung, liver, skeletal muscle, kidney, pancreas, cerebellum, cerebral cortex and medulla (in microglia as well as in astrocytes), brain microvascular, coronary artery and umbilical cord endothelial cells. Isoform 1 is predominant in all tissues tested.
CC CC
CC -1- PM: SULFATED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
QY Query Match 45.0%; Score 49; DB 1; Length 352;
Bst Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Db 1 IIITSLIGGLIIII 17
47 IIFLGIIVGNGLVLM 63
RESULT 9
CCR4_MACEA STANDARD; PRT; 352 AA.
ID CCR4_MACEA
AC Q28474;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor) (Stromal cell-derived factor 1 receptor) (Fusin) (LBSTR).
GN CXCR4.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; OC Cercopithecinae; Macaca.
CX NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (JUL-1996) to FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
```


CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D86579; BAA13126.1; -.
DR PIR; G00048; G00048.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 39
FT TRANSMEM 40 63
FT DOMAIN 64 79
FT TRANSMEM 80 99
FT DOMAIN 100 110
FT TRANSMEM 111 132
FT DOMAIN 133 154
FT TRANSMEM 155 175
FT DOMAIN 176 200
FT TRANSMEM 201 220
FT DOMAIN 221 240
FT TRANSMEM 241 261
FT DOMAIN 262 285
FT TRANSMEM 286 305
FT DOMAIN 306 352
FT MOD RES 21 21
FT CARBOHYD 11 11
FT DISULFID 109 186
SQ SEQUENCE 352 AA; 39753 MW; 432DA6C11859EF8A CRC64;

Query Match 45.0%; Score 49; DB 1; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17
Db 47 IIFLGIIVNGVLIVM 63

RESULT 10
CCRA_MACMU STANDARD; PRT; 352 AA.
AC P79394; 002745; 046428;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)
DE (Stromal cell-derived factor 1 receptor) (Fusin) (LESTR).
GN CXCR4.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Carcophoridae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Indian macaque; PubMed=9060623;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry.";
RL U. Virol. 71:2705-2714(1997).
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.-H., Clements J.E., Murphy-Corb M.,
RA Pelzer S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Chinese;
RX MEDLINE=98252393; PubMed=9591719;
RA Prefet J.-L., Guillet J.-G., Butor C.;
RT "New widespread CXCR4 allele in rhesus macaques does not predict
RT subspecies or clinical evolution.";
RL AIDS Res. Hum. Retroviruses 14:639-641(1998).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U73740; AAC51159.1; -.
DR EMBL; U93311; AAB54116.1; -.
DR InterPro; IPR001928; AAC39641.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 39
FT TRANSMEM 40 63
FT DOMAIN 64 79
FT TRANSMEM 80 99
FT DOMAIN 100 110
FT TRANSMEM 111 132
FT DOMAIN 133 154
FT TRANSMEM 155 175
FT DOMAIN 176 200
FT TRANSMEM 201 220
FT DOMAIN 221 240
FT TRANSMEM 241 261
FT TRANSMEM 262 285
FT TRANSMEM 286 305
FT DOMAIN 306 352
FT MOD RES 21 21
FT CARBOHYD 11 11
FT DISULFID 109 186
FT CONFLICT 67 67
FT CONFLICT 214 214
FT CONFLICT 348 348
SQ SEQUENCE 352 AA; 39739 MW; EC415E4820699C3F CRC64;

Query Match 45.0%; Score 49; DB 1; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGGLILII 17
Db 47 IIFLGIIVNGVLIVM 63

RESULT 11
CCRA_PAPAN

ID CCR4_PAPAN STANDARD; PRT; 352 AA.
AC P56491;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)
DE (Stromal cell-derived factor 1 receptor) (Fusin).
GN CXCR4.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OC NCBI_TaxID=9555;
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCE A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC or send an email to license@isb-sib.ch).

DR EMBL; AF031089; AAC63831.1; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 39
FT TRANSSEM 40 63
FT TRANSSEM 64 79
FT TRANSSEM 80 99
FT DOMAIN 100 110
FT TRANSSEM 111 132
FT DOMAIN 133 154
FT TRANSSEM 155 175
FT DOMAIN 176 200
FT TRANSSEM 201 220
FT DOMAIN 221 240
FT TRANSSEM 241 261
FT DOMAIN 262 285
FT TRANSSEM 286 305
FT DOMAIN 306 352
FT MOD_RES 21 21
FT CARBOHYD 11 11
FT DISULFID 109 186
SQ SEQUENCE 352 AA; 39751 MW; 468542E1851265A CRC64;
Query Match 45.0%; Score 49; DB 1; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

DT 26-FEB-2003 (Rel. 41, Last annotation update)
DE C-X-C chemokine receptor type 4 (CXCR-4) (SDF-1 receptor)
DE (Stromal cell-derived factor 1 receptor) (Fusin) (Leukocyte-derived
DE seven transmembrane domain receptor) (LESTR) (LCR1).
GN CXCR4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Locus coeruleus;
RX MEDLINE=94052833; PubMed=8234909;
RA Rimland J., Xin W., Sweetnam P., Sajjoh K., Neetler E.J., Duman R.S.;
RT "Sequence and expression of a neuropeptide Y receptor cDNA.";
RL Mol. Pharmacol. 40:869-875(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Werling D.;
RT "Role of chemokines in respiratory syncytial virus infection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SHOWS THAT IT IS NOT A NPY3-R.
RX MEDLINE=94052833; PubMed=8234909;
RA Jazin E.E., Yoo H., Blomqvist G., Yee F., Weng G., Walker M.W.,
RA Salan J., Lathamer D., Mahlestedt C.R.;
RT "A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its
RT human homologue, confers neither NPY binding sites nor NPY
RT responsiveness on transfected cells.";
RL Regul. Pept. 47:247-258(1993).
CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCE A
CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, HEART, KIDNEY, LONG AND LIVER.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- CAUTION: Was originally (Ref.1) thought to be a receptor for
CC neuropeptide Y type 3 (NPY3-R).

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DR EMBL; M66739; -; NOT ANNOTATED_CDS.
DR EMBL; AF399642; AAK94452.1; -
DR PIR; S28787; S28787.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 40
FT TRANSSEM 41 64
FT DOMAIN 65 80
FT TRANSSEM 81 100
FT DOMAIN 101 111
FT TRANSSEM 112 133
FT DOMAIN 134 155
FT TRANSSEM 156 176
FT DOMAIN 177 201
FT TRANSSEM 202 221
FT DOMAIN 222 241
FT TRANSSEM 242 262
FT DOMAIN 263 286
FT TRANSSEM 287 306
FT DOMAIN 307 353
FT MOD_RES 22 22
SQ SEQUENCE 352 AA; 39751 MW; 468542E1851265A CRC64;
Query Match 45.0%; Score 49; DB 1; Length 352;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

RC STRAIN=C57BL/6J x CBA; TISSUE=Thymus;
 RX MEDLINE=97439495; PubMed=9295051;
 RA Moeppe B., Frodl R., Rodewald H.-R., Baggiolini M., Gierschik P.;
 RT "Two murine homologues of the human chemokine receptor CXCR4 mediating
 RT stromal cell-derived factor 1alpha activation of G12 are
 RT differentially expressed in vivo.";
 RL Eur. J. Immunol. 27:2102-2112(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS CXCR4-A AND CXCR4-B).
 RX MEDLINE=97256574; PubMed=9103415;
 RA Heesen M., Berman M.A., Hoepken U.E., Gerard N.P., Dorf M.E.;
 RT "Alternate splicing of mouse fusin/CXC chemokine receptor-4: stromal
 RT cell-derived factor-1alpha is a ligand for both CXC chemokine
 RT receptor-4 isoforms.";
 RL J. Immunol. 158:3561-3564(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM CXCR4-B).
 RC STRAIN=C57BL/6; TISSUE=Thymus;
 RA Suzuki G., Nakata Y., Uza A., Shirasawa T., Saito T., Mita K.;
 RL Submitted (EBB-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=99095114; PubMed=9879064;
 RA Frodl R., Gierschik P., Moeppe B.;
 RT "Genomic organization and expression of the CXCR4 gene in mouse and
 RT man: absence of a splice variant corresponding to mouse CXCR4-B in
 RT human tissues.";
 RL J. Recept. Signal Transduct. Res. 18:321-344(1998).
 RN [8]
 RP FUNCTION.
 RX MEDLINE=98295994; PubMed=9634237;
 RA Techibana K., Hirota S., Iizasa H., Yoshida H., Kawabata K.,
 RA Katsuka Y., Kitemura Y., Matsushima K., Yoshida N., Nishikawa S.-I.,
 RA Kishimoto T., Nagasawa T.;
 RT "The chemokine receptor CXCR4 is essential for vascularization of the
 RT gastrointestinal tract.";
 RL Nature 393:591-594(1998).
 RN [9]
 RP FUNCTION.
 RX MEDLINE=98295995; PubMed=9634238;
 RA Zou Y.-R., Kottmann A.H., Kuroda M., Taniuchi I., Littman D.R.;
 RT "Function of the chemokine receptor CXCR4 in hematopoiesis and in
 RT cerebellar development.";
 RL Nature 393:595-599(1998).
 RN [10]
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=ICR;
 RX MEDLINE=99410349; PubMed=10479460;
 RA McGrath K.E., Koniski A.D., Maleby K.M., McGann J.K., Palis J.;
 RT "Embryonic expression and function of the chemokine SDF-1 and its
 RT receptor, CXCR4.";
 RL Dev. Biol. 213:442-456(1999).
 CC -1- FUNCTION: RECEPTOR FOR THE C-X-C CHEMOKINE SDF-1. TRANSDUCES A
 CC SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
 CC INVOLVED IN B-CELL LYMPHOPOIESIS, BONE-MARROW MYELOPOIESIS AND IN
 CC CARDIAC VENTRICULAR SEPTUM FORMATION. PLAYS ALSO AN ESSENTIAL ROLE
 CC IN VASCULARIZATION OF THE GASTROINTESTINAL TRACT. PROBABLY BY
 CC REGULATING VASCULAR BRANCHING AND/OR REMODELLING PROCESSES IN
 CC ENDOTHELIAL CELLS. INVOLVED IN CEREBELLAR NEURONAL LAYER
 CC FORMATION, PREVENTING PREMATURE MIGRATION OF PROLIFERATING GRANULE
 CC CELLS FROM THE EXTERNAL GRANULAR LAYER INWARDS. IN THE CNS, COULD
 CC MEDIATE HIPOCAMPAL-NEURON SURVIVAL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=CXCR4-B; Synonyms=LESTR-B;
 CC IsoId=P70658-1; Sequence=Displayed;
 CC Name=CXCR4-A; Synonyms=LESTR-A;
 CC IsoId=P70658-2; Sequence=VSP_001891;
 CC -1- TISSUE SPECIFICITY: LYMPHOCTES, MACROPHAGES, NEUTROPHILS,
 CC MICROGLIAL CELLS AND ASTROCYTES. FOUND IN SPLEEN, THYMUS, BONE
 CC MARROW, LYMPH NODES AND, AT LOWER LEVELS IN BRAIN, SMALL
 CC INTESTINE, STOMACH AND KIDNEY. CXCR4-A IS PREDOMINANT IN ALL

CC TISSUES TESTED.
 CC -1- DEVELOPMENTAL STAGE: HIGH EXPRESSION DURING EMBRYONIC DEVELOPMENT
 CC DOES NOT SEEM TO BE ASSOCIATED WITH THE DIFFERENTIATION OF ANY
 CC PARTICULAR CELL TYPE, BUT IS WIDELY UTILIZED WHEN THERE IS A
 CC REQUIREMENT FOR CELL MOVEMENT. FREQUENTLY ASSOCIATED WITH LESS
 CC DIFFERENTIATED CELL TYPES AND DOWN-REGULATED WITH SUBSEQUENT
 CC DIFFERENTIATION. DETECTED IN SITES WITH HAEMOPOIETIC POTENTIAL:
 CC THE YOLK SAC (7.5, 8.5 AND 12.5 DPC) AND FETAL LIVER (12.5 DPC).
 CC DURING GASTRULATION. AT 7.2 TO 7.8 DPC, EXPRESSED IN THE MESODERM
 CC AND THE DERIVATIVE ENDODERM. AS GASTRULATION PATTERN PADS (8.5
 CC DPC), EXPRESSION IN THE MESODERM IS DOWN-REGULATED, WHILE IT
 CC BECOMES PREDOMINANT IN NEURAL ECTODERM. ENDODERMAL EXPRESSION IS
 CC RETAINED IN THE FOREGUT AND LATER IN A SUBSET OF FOREGUT
 CC DERIVATIVES, INCLUDING THE STOMACH (10.5 DPC), THE CYSTIC DUCTS OF
 CC THE GALLBLADDER AND THE LUNG EPITHELIUM (12.5 DPC). IN NEURONAL
 CC TISSUE: AT 10.5 AND 12.5 DPC, EXPRESSED IN THE DORSAL ROOT
 CC GANGLIA, IN THE VENTRAL MANTLE LAYER OF THE SPINAL CORD (OR BASAL
 CC PLATES), IN THE HINDRAIN. AT 14.5 DPC, EXPRESSION MORE TIGHTLY
 CC CONFINED TO THE NEURAL EPITHELIUM LINING THE VENTRICULAR SPACE AND
 CC TO THE EXTERNAL GRANULAR LAYER OF THE VENTRAL RHOMBIC LIP (THE
 CC DEVELOPING CEREBELLUM). EXPRESSED IN THE OUTPOCKETING OF THE
 CC DIVERGENT FLOOR AT 10.5 DPC AND IN THE DEVELOPING THALAMUS AND,
 CC TO A LESSER EXTENT, THE DEVELOPING HIPOTHALAMUS. AT 14.5 DPC,
 CC RESTRICTED TO THE REGION WHERE THALAMUS AND HYPOTHALAMUS MEET.
 CC DETECTED IN A DISCRETE BAND OF CELLS AT THE EDGE OF THE OLFACTORY
 CC BULB. IN THE VASCULAR SYSTEM: EXPRESSED IN THE ENDOTHELIUM OF
 CC NUMEROUS BLOOD VESSELS, BUT NOT ALL, AT 10.5, 11.5 AND 12.5 DPC,
 CC SUCH AS VITELLINE/UMBILICAL VESSELS, CARDIAC VENTRICULAR WALL
 CC CAPILLARIES, FACIAL VESSELS AND, AT 14.5 DPC, IN THE VASCULATURE
 CC OF THE HERNIATED GUT. EXPRESSION SEEMS TO BE ASSOCIATED WITH
 CC EXPANDING VASCULAR NETWORKS. IN THE HEART DEVELOPMENT, EXPRESSED
 CC AT 10.5 DPC IN THE PRECURSOR. IN THE AOROPULMONARY (AP) SEPTUM. AT
 CC 12.5 DPC, DETECTED IN THE AP SEPTUM AT THE BASE OF THE OUTFLOW
 CC TRACT AND IN THE ATRIOVENTRICULAR VALVES. DETECTED IN CRANOFACIAL
 CC ECTODERM FROM 10.5 TO 14.5 DPC. AT 10.5 AND 11.5 DPC, EXPRESSED IN
 CC THE RATHEKE'S POUCH.
 CC -1- PTM: SULFATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; U59760; AAB07725.1; -
 CC EMBL; U65580; AAC52953.1; -
 CC EMBL; D87747; BAA13451.1; -
 CC EMBL; Z80111; CAB02201.1; -
 CC EMBL; Z80112; CAB02202.1; -
 CC EMBL; X9581; CAA67893.1; -
 CC EMBL; X9582; CAA67894.1; -
 CC EMBL; AB000803; BAA19187.1; -
 CC MGD; MG1:109563; CXCR4.
 CC GO; GO:0007420; P:brain development; IMP.
 CC GO; GO:0030334; P:regulation of cell migration; IMP.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSIN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 CC KMW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 CC Alternative splicing;
 CC KW DOMAIN 1 41
 CC FT DOMAIN 1 41
 CC FT TRANSMEM 42 65
 CC FT DOMAIN 66 81
 CC FT TRANSMEM 82 101
 CC FT DOMAIN 102 112
 CC FT TRANSMEM 113 134
 CC FT DOMAIN 135 156
 CC FT TRANSMEM 157 177
 CC EXTRACELLULAR (POTENTIAL).
 CC 1 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 2 (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC 3 (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC 4 (POTENTIAL).

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FT DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 208 227 5 (POTENTIAL).
FT DOMAIN 228 247 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 248 268 6 (POTENTIAL).
FT DOMAIN 269 292 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 293 312 7 (POTENTIAL).
FT DOMAIN 313 359 CYTOPLASMIC (POTENTIAL).
FT DISULFID 111 193 BY SIMILARITY.
FT MOD RES 23 23 SULFATION (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 6 7 Missing (in isoform CXCR4-A).
FT CONFLICT 216 216 /FTId=VSP_001891.
SQ SEQUENCE 359 AA; 40426 MW; 33D1B552A31595B CRC64;

Query Match 45.0%; Score 49; DB 1; Length 359;
Best Local Similarity 47.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 IILITSLIGGLILII 17
Db 49 IIFLTGIVNGVLIVM 65

```

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RESULT 15
YC48 HAEIN STANDARD; PRT; 322 AA.
AC P44136;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein H11248.
GN H11248.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; Pubmed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Klevavage A.R., Bult C.J., Tomb J.-F., Dougherty B.B., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudex D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,
RA Gnehm C.B., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: SOME, TO E.COLI YOHM AND M.JANNASCHII M1092.
CC
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL, U32805; AAC22907.1; -.
DR DR PIR; A64023; A64023.
DR TIGR; H11248; -.
KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 7 27 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 228 248 POTENTIAL.

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FT TRANSMEM 294 314 POTENTIAL.
SQ SEQUENCE 322 AA; 35669 MW; EC1248D2F25A1F47 CRC64;

Query Match 43.1%; Score 47; DB 1; Length 322;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 4 ITSLIGGLILIIIVVVG 23
Db 291 IYKLIAGIMLPFALSILYG 310

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 Job time : 2.82423 secs

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OM protein - protein search, using sw model

Run on: August 18, 2003, 13:13:47 ; Search time 8.49406 Seconds
(without alignments)
729.128 Million cell updates/sec

Title: US-09-892-949-2_COPY_520_543
Perfect score: 109
Sequence: 1 ILITSLIGGGLILILITVAYGL 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	732	4	Q8N117
2	83	76.1	235	11	Q8BSU3
3	83	76.1	716	11	Q8K5B1
4	83	76.1	716	11	Q8R501
5	52	47.7	314	11	Q8VGY3
6	52	47.7	527	17	Q9YBL7
7	52	47.7	795	5	Q9XZF9
8	52	47.7	795	5	Q9VUX9
9	52	47.7	795	5	Q9NBK8
10	51	46.8	97	16	Q9RUV1
11	51	46.8	163	2	Q9ZSV8
12	51	46.8	206	16	Q9SZM5
13	51	46.8	254	16	Q8RI00
14	51	46.8	288	16	Q8KGC3
15	51	46.8	314	4	Q8NGK2
16	51	46.8	465	16	Q9A4R5

17	51	46.8	530	16	Q9KRU9	Q9KRU9 vibrio chol
18	50.5	46.3	580	16	P74642	P74642 synechocyst
19	50	45.9	366	17	Q58596	Q58596 methanococc
20	49.5	45.4	233	16	Q8CV70	Q8CV70 oceanobactil
21	49.5	45.4	363	16	Q8NP90	Q8NP90 corynebacte
22	49	45.0	270	4	Q8NGM6	Q8NGM6 homo sapien
23	49	45.0	284	16	Q9ZMS2	Q9ZMS2 rhizobium m
24	49	45.0	272	16	Q8EWI7	Q8EWI7 mycoplasma
25	49	45.0	301	8	Q950G6	Q950G6 spitzellomyc
26	49	45.0	306	11	Q8VGP1	Q8VGP1 mus musculu
27	49	45.0	331	17	Q9H24	Q9H24 thermoplas
28	49	45.0	332	11	Q62973	Q62973 ratius norv
29	49	45.0	334	6	Q9N130	Q9N130 salmistri bol
30	49	45.0	334	6	Q9N1P2	Q9N1P2 saguinus oe
31	49	45.0	334	6	Q9N1P4	Q9N1P4 cercopithec
32	49	45.0	334	6	Q9N1P3	Q9N1P3 hylobates l
33	49	45.0	346	6	Q9WZM2	Q9WZM2 nycticebus
34	49	45.0	346	6	Q9WZM3	Q9WZM3 nycticebus
35	49	45.0	346	6	Q9WZM4	Q9WZM4 nycticebus
36	49	45.0	347	6	Q9WZP2	Q9WZP2 mandrillus
37	49	45.0	347	6	Q9WZM6	Q9WZM6 hylobates c
38	49	45.0	347	6	Q9WZP8	Q9WZP8 colobus pol
39	49	45.0	347	6	Q9WZP1	Q9WZP1 mandrillus
40	49	45.0	347	6	Q9WZQ0	Q9WZQ0 pygathrix n
41	49	45.0	347	6	Q9WZM1	Q9WZM1 eulemur mac
42	49	45.0	347	6	Q9WZM5	Q9WZM5 pithecia pi
43	49	45.0	347	6	Q9WZP0	Q9WZP0 macaca asse
44	49	45.0	347	6	Q9WZM8	Q9WZM8 callithrix
45	49	45.0	347	6	Q9WZM0	Q9WZM0 alouatta se

ALIGNMENTS

RESULT 1	Q8N117	PRELIMINARY;	PRT;	732 AA.
ID	Q8N117			
AC	Q8N117;			
DT	01-OCT-2002 (TRMBLrel. 22, Created)			
DT	01-OCT-2002 (TRMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TRMBLrel. 23, Last annotation update)			
DE	Gp130-like monocyte receptor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2198187; PubMed=11877449;			
RA	Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.;			
RT	"A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals			
RT	Proliferation, and Activates STAT-3 and STAT-5."			
RL	J. Biol. Chem. 277:16831-16836(2002).			
DR	EMBL; AF486620; AAM27958.1; -.			
DR	InterPro; IPR002996; CR1A.			
DR	InterPro; IPR003961; FN_III.			
DR	SMART; SM00060; FN3; 3.			
KW	Receptor.			
SQ	SEQUENCE 732 AA; 82953 MW; 30F84BD3DD9A20E CRC64;			
Query Match	100.0%; Score 109; DB 4; Length 732;			
Best Local Similarity	100.0%; Pred. No. 5.3e-06;			
Matches 24; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 ILITSLIGGGLILILITVAYGL 24			
DB	520 ILITSLIGGGLILILITVAYGL 543			
RESULT 2	Q8BSU3	PRELIMINARY;	PRT;	235 AA.
ID	Q8BSU3			

AC OBB8U3; (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Plutitary;
 RC MEDLINE=22354683; PubMed=12466831;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL: AK030512; BAC26998.1; -.
 KM Hypothetical protein.
 QO SEQUENCE 235 AA; 25133 MW; 50928397A1AD126F CRC64;

Query Match	76.1%	Score 83	DB 11	Length 235
Best Local Similarity	66.7%	Pred. No. 0.0043		
Matches 16	Conservative	5	Mismatches 3	Indels 0
			Gaps	0

Qy	Db
1 IILITSLIGGGLLIILITVAYGL 24	26 IVLITSLVGGGLLLSIKIVTFFGL 49

RESULT 3	
Q8K5B1	
ID Q8K5B1	PRELIMINARY;
	PRT; 716 AA

DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Gp130-like monocyte receptor.
GN GLMR.
OS Mus musculus (Mouse).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21981817; PubMed=11877449;
RA Ghilardi N., Li J., Hongo J.A., Yi S., Gurney A., De Sauvage F.J.,
RT "A Novel Type I Cytokine Receptor Is Expressed on Monocytes, Signals
RT Proliferation, and Activates STAT-3 and STAT-5." ,
RL J. Biol. Chem. 277:15831-16836(2002).
DR EMBL; AF486621; F04827959.1; -.
DR MGD; MGI:2180511; Glmr.
DR InterPro; IPR002996; CRA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3.1.
DR SMART; SM00060; FN3.3.
KW Receptor.
QO SEQUENCE. 716 AA; 80641 MW; 3956B0B253F7C7B5 CRC64;

Query Match Similarity 76.1%; Score 83; DB 11; Length 716;
 Best Local Similarity 66.7%; Pred. No. 0.011;
 Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 ILITSLIGGGLIPIILTVAYGL 24
|::||::||::||::||
Db 507 IVLLTSLVGGGLLSIKVTFTGL 530

RESULT 4	
Q8R501	
ID Q8R501	PRELIMINARY;
AC Q8R501;	PRT; 716 AA

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01-UNN-2002 (TREMBLrel. 21, Created)
DT 01-UNN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Cytokine receptor NR10.
GN GMR OR NR10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP
RC
RC STRAIN=C57BL/6;
RA Nomura H., Yaguchi N., Maeda M., Hasegawa M.;
RT "Polymorphism between C57BL/6 and Balb/c in the novel cytokine
RT receptor NR10."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083111; BAB88745.1; -.
DR MGD; MGI:2180511; Gmr.
DR InterPro; IPR002966; CRIA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; FN3; 1.
DR SMART; SM0060; FN3; 3.
KW Receptor.
SQ
SEQUENCE 716 AA; 80598 MW; CBBP718DCCD40FCT CRC64;
Query Match 76.1%; Score 83; DB 11; Length 716;
Best Local Similarity 66.7%; Pred.No. 0.011;
Matches 16; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
1 IILITSLGGGLILITLITVAYGL 24
I:::|||||::|::|::|::|
507 IVLITSLVGGGLILITSLIKTVFGL 530

```

Query Match	76.1%	Score 83;	DB 11;	Length 716;
Best Local Similarity	66.7%	Pred. No. 0.011;		
Matches 16; Conservative	5;	Mismatches 3;	Indels 0;	Gaps 0;

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QY      1 ILLTSLGGGLLILLLTVANGL 24
          |::|||:||||:|:|:|
Db      507 IVLLTSLVGGGLLLSIKVTFFGL 530

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RESULT 5	
Q8VGY3	
ID Q8VGY3	PRELIMINARY; PRT; 314 AA

01-MAR-2002 (TREMblrel. 20, Created)
 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 Olfactory receptor MOR31-4.
 Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY073007; AAL06070.1; -
 DR InterPro: IPR000276; GPCR_Rhodopn.
 DR Pfam: PF00001; 7cm_1; 1.
 DR PRINTS: PR00237; GPCRRHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECCEP_FL_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECCEP_FL_2; 1.
 RN Receptor. 314 AA; 3553 MW; 5308508BD931B80E CRC64;
 SQ SEQUENCE

Query Match	47.7%	Score 52	DB 11	Length 314
Best Local Similarity	63.2%	Pred. NC	53	
Matches 12	Conservative 2	Mismatches 5	Indels 0	Gaps 0

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QY      1 IILTSLIGGGLLIILT 19
        | | | : | | | | |
Db      35 ISYITALGNSLLFIILT 53
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RESULT 6
Q9YBL7 PRELIMINARY; PRT; 527 AA.
AC Q9YBL7;
DT 01-NOV-1999 (TRMBLrel. 12, Created)
DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)
DE 527AA long hypothetical oligopeptide transport system permease
DE protein.
GN APE1581.
OS Aeropyrum pernix.
OC Archaea; Ctenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatakeyama Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000062; BAA80581.1; -
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR000566; Lipocin_cycFMBP.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Complete proteome.
SQ SEQUENCE 527 AA; 57790 MW; 9120E07F292D6AE1 CRC64;

Query Match 47.7%; Score 52; DB 17; Length 527;
Best Local Similarity 40.9%; Pred. No. 83;
Matches 9; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLLIILITLVAY 22
Db 375 LILFAIIGGNIWILFIVAF 396

RESULT 7
Q9XZF9 PRELIMINARY; PRT; 795 AA.
AC Q9XZF9;
DT 01-NOV-1999 (TRMBLrel. 12, Created)
DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)
DE 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE TOLL like protein.
GN TEHAO OR CG7121.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RA Luo C., Zheng L.;
RT "Toll and related proteins from insects."
RT Submitted (APR-1999) to the EMBL/GenBank/DBD databases.
DR EMBL; AF140019; AAD30131.1; -
DR HSP; G60603; IFTW.
DR Flybase; FBgn0026760; Tehao.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR001611; LRR-
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00560; LRR; 5.

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DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTERKLRIE.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 1.
DR PROSITE; PS50104; TIR; 1.
SQ SEQUENCE 795 AA; 90256 MW; 32288BC66A86E249 CRC64;

Query Match 47.7%; Score 52; DB 5; Length 795;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLLIILITLVAY 22
Db 591 VLLISCVGGLVIVICLLTVF 612

RESULT 8
Q9VUX9 PRELIMINARY; PRT; 795 AA.
AC Q9VUX9;
DT 01-MAY-2000 (TRMBLrel. 13, Created)
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
DE TEHAO protein.
GN TEHAO OR CG7121.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Mohtrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Patel J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard Y., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Turner R.,
RA Svikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003640; AAF53306.1; -.
DR HSSP; O60603; 1FVW.
DR FlyBase; FBgn026760; Tshao.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00560; LRR_5.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 1.
DR PROSITE; PS50104; TIR; 1.
SQ SEQUENCE 795 AA; 90241 MW; 61B8839E2036E28C CRC64;

Query Match 47.7%; Score 52; DB 5; Length 795;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

OY 1 IILITSLGGGLIILITVAV 22
DB 591 VLLISCVGGLVIVICLIVFY 612

RESULT 9

O9NBK8 PRELIMINARY; PRT; 795 AA.
AC O9NBK8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Toll-5.
GN TEHAO OR CG7121.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Tauszig S., Jouanguy E., Hoffmann J., Imler J.L.;
RT "Toll-related receptors and the control of antimicrobial peptide
expression in *Drosophila*.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2000).
DR EMBL; AF247767; AAF66227.1; -.
DR HSSP; O60603; 1FVW.
DR FlyBase; FBgn026760; Tshao.
DR InterPro; IPR004075; IL1_receptor1.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR_domain.
DR Pfam; PF00560; LRR_5.
DR Pfam; PF01462; LRRNT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO1537; INTRLNRI1F.
DR PRINTS; PRO0019; LEURICHRPT.
DR SMART; SM00013; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 1.
DR PROSITE; PS50104; TIR; 1.
SQ SEQUENCE 795 AA; 90255 MW; 3A0883EE4A6E247 CRC64;

Query Match 47.7%; Score 52; DB 5; Length 795;

Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

OY 1 IILITSLGGGLIILITVAV 22
DB 591 VLLISCVGGLVIVICLIVFY 612

RESULT 10

O9RUV1 PRELIMINARY; PRT; 97 AA.
AC O9RUV1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein DR1280.
GN DR1280.
OS *Deinococcus radiodurans*.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxId=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Ueberlack T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium *Deinococcus*
RT *radiodurans* RI.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001975; AAF10855.1; -.
DR TIGR; DR1280; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 97 AA; 10260 MW; 1784AF3FFCD5F16 CRC64;

Query Match 46.8%; Score 51; DB 16; Length 97;
Best Local Similarity 41.7%; Pred. No. 25;
Matches 10; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 1 IILITSLGGGLIILITVAVGL 24
DB 67 IYILGFLVGSGLVALVALAAVGL 90

RESULT 11

O9ZSV8 PRELIMINARY; PRT; 163 AA.
AC O9ZSV8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Hypothetical 16.4 kDa protein (Fragment).
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycaceae;
OX NCBI_TaxId=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cadwallader A.B., McCormick J.R.;
RT "Identification and Characterization of the Cell Division Gene *ftsI* of
RT *Streptomyces coelicolor* A3(2).";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF123319; AAD20009.1; -.
DR InterPro; IPR002965; P-rich_extensn.
DR PRINTS; PRO1217; PRICHEXTENSN.
KW Hypothetical protein.
FT NON_TER 1

SO SEQUENCE 163 AA; 16354 MW; 09ED9F39D9514B5E CRC64;

Query Match 46.8%; Score 51; DB 2; Length 163;
Best Local Similarity 42.9%; Pred. No. 40;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLLILITVA 21
12 VLLVVLGGGLIGLIVLNSA 32

RESULT 12

Q9S2W5 PRELIMINARY; PRT; 206 AA.

AC Q9S2W5; PRELIMINARY; PRT; 206 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Putative membrane protein.
GN SC02091 OR SC4A10.24C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteriae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;

RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D.C., Harris D.,
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kleser H.M., Denapalae D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RL "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA MEDLINE=2196410; PubMed=1200953;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)." ;
RL Nature 417:141-147 (2002).
DR EMBL; AL939111; CAB52000.1; -
DR InterPro; IPR002965; P rich extensn.
DR PRINTS; PRO1217; PRICHEXTENS.
KW Complete proteome.
SQ SEQUENCE 206 AA; 20899 MW; 90131DF9AAB05D7 CRC64;

Query Match 46.8%; Score 51; DB 16; Length 206;
Best Local Similarity 42.9%; Pred. No. 49;
Matches 9; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 ILITSLIGGGLLILITVA 21
55 VLLVVLGGGLIGLIVLNSA 75

RESULT 13
Q8RI00 PRELIMINARY; PRT; 254 AA.

AC Q8RI00; PRELIMINARY; PRT; 254 AA.
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Glycerol uptake facilitator protein.
GN FN1838.

OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriae; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
NCBI_TaxID=76856;

RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=1189109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykdis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
RA Larsen N., d'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fontein M., Kyriades N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018 (2002).
DR EMBL; AE010486; AAL93937.1; -
DR InterPro; IPR00425; MIP_family.
DR Pfam; PF00230; MIP; 1.
DR ProDom; PD000295; MIP_family; 1.
DR TIGRFAMs; TIGR00861; MIP; 1.
DR PROSITE; PS00221; MIP; 1.
KW Complete proteome.

SO SEQUENCE 254 AA; 26879 MW; 8A2618C889339CB2 CRC64;
Query Match 46.8%; Score 51; DB 16; Length 254;
Best Local Similarity 38.1%; Pred. No. 59;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 3 ILITSLIGGGLLILITVYG 23
148 IVTEITIGLILIGLIVLNSA 168

RESULT 14
Q8KGC3 PRELIMINARY; PRT; 288 AA.

AC Q8KGC3; PRELIMINARY; PRT; 288 AA.
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein CT0045.
GN CT0045.

OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
NCBI_TaxID=1097;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwin M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathavan J., Khouir H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TUS, a
phototrophic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
DR EMBL; AE012784; AAM71293.1; -
DR TIGR; CT0045; -

DR InterPro; IPR000276; GPCR_Rhodsp.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1, 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 288 AA; 32122 MW; 4A5E26101B84C9F9_CRC64

Query Match	46.8%	Score 51	DB 16	Length 288
Best Local Similarity	41.7%	Pred. No. 66		
Matches 10	Conservative 6	Mismatches 8	Indels 0	Gaps 0

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QY      1 IILTSLIGGGLILILITVAYGL 24
          ::: ||||| ::|||
Db      129 VLFMLAYAGGLILFLLGVYRL 152

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RESULT 15

ID	08NGK2	PRELIMINARY;	PRT;	314 AA.
AC	08NGK2;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DS	Seven transmembrane helix receptor.			
OS	Homo sapiens (Human) .			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RA	Swara M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,			
RA	Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;			
RT	"Genome-wide discovery and analysis of human seven transmembrane helix			
RT	receptor genes";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB065792; BAC06011.1; -			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; Tm_1; 1.			
DR	PRINTS; PR00237; GPCRHOOPS.			
DR	PROSITE; PS50262; G PROTEIN_RECPT_FL_2; 1.			
KW	Receptor; Transmembrane.			
SO	SEQUENCE 314 AA; 35622 MW; 001831FCAA557474 CRC64;			

Query Match 46.8%; Score 51; DB 4; Length 314;
 Best Local Similarity 57.9%; Pred. No. 71;
 Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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QY      1 ILITSLIGGGLLIILT 19
        | :|:|:| | | | |
Db      35 ISVTALIGNSLLFIILT 53
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Job time : 9.49406 secs